- protein search, using sw model

OM protein

. March Run on:

2, 2006, 00:31:42 ; Search time 206.5 Seconds
(without alignments)
917.057 Million cell updates/sec

US-08-981-087B-1 2288 1 SYTNDKILILYFNKLYKKIK.....TSSNGCFWSFISKEHGWQEN 431 Title: Perfect score:

Scoring table:

Sequence:

2443163 segs, 439378781 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2004s:\* geneseqp2005s:\* geneseqp1980s:\* geneseqp2002s: geneseqp1990s: geneseqp2000s: geneseqp2001s: A\_Geneseq\_ Database

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P					
Result No.	Score	Query Match Length DB	Leng	yth D	щ	ΩI	Description
-	2288	100.0		431	2	AAW09014	
7	2288	100.0		432	4	AAB04103	
m	2288	100.0		432	4	AAB04096	
4	2288	100.0		645	4	AAE07894	_
ഹ	2288	100.0		645	ý	AAE35692	
9	2288	100.0		657	ø	AAE35693	
7	2288	100.0		657	ø	AAE35694	
æ	2288	100.0		685	4	AAE07893	
σ	2288	100.0		862	4	AAE07890	
10	2288	100.0		887	4	AAE07892	
11	2288	100.0		979	9	AAE35713	
12	2288	100.0	7	032	4	AAE07901	Aae07901 C. botuli
13	2288	100.0	_	059	ო	AAY93309	Aay93309 A mangane
14	2288	100.0	***	084	ო	AAY93312	
15	2288	100.0		092	4	AAE07900	
16	2288	100.0	_	192	9	AAE35711	Aae35711 BONT/F-HC
17	2288	100.0	_	192	G	AAE35710	
18	2271	99.3		432	٣	AAY77138	Aay77138 Synthetic
19	1800	78.7	_	448	~	AAW68399	
20	1451.5	63.4		449	٣	AAY77137	Aay77137 Synthetic
21	1451.5	63.4		449	4	AAB04094	Aab04094 Botulism
22	1447.5	63.3		452	~	AAW68396	Aaw68396 Clostridi
23	1426	62.3		451	~	AAW68395	Aaw68395 Clostridi
24	1423.5	62.2		419	4	AAB04095	Aab04095 Botulism

	4 <b>4</b>		Adwilosa Full leng Adz36018 C. botuli	_		_	٠.		Aar95008 Type A ne		٠,	Aaw68391 Clostridi	Aar95009 Type A ne	Aaw68390 Clostridi	Aab04089 Botulism	Aab04090 Botulism	Aay77140 Native bo
AAE07898 ADZ69764	AAY93307 AAY93310	AAR95010	ADW11038 ADZ36018	ADZ60275	ADZ69730	ADZ69729	ADZ69831	AAB04088	AAR95008	AAW68389	AAY77134	AAW68391	AAR95009	AAW68390	AAB04089	AAB04090	AAY77140
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BoBT/F; immunogen; vaccine; botulism. Immunogenic type F botulinum toxin heavy chain (aa848-1278). Clostridium botulinum; type F strain Langeland AAW09014 standard; protein; 431 AA 96WO-GB001409. Botulinum toxin; neurotoxin; (revised)
(first entry) 27-DEC-1996. WO9641881-A1. 12-JUN-1996; 17-OCT-2003 31-MAR-1997 AAW09014; AAW09014 

BEST AVAILABLE CO

95GB-00011909. 12-JUN-1995;

Minton NP, (MICR-) MICROBIOLOGICAL RES AUTHORITY. Elmore MJ, Mauchline ML,

Pasechnik VA;

WPI; 1997-065467/06. N-PSDB; AAT48100

Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.

Claim 5; Page 16-17; 37pp; English.

A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278) of a type F botulinum neurotoxin (BoNT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine produ. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field) the heavy chain. The polypeptides and its fragments (see also 19015-17) lack the light chain and HN epitopes necessary for

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Disclosure; Fig 18b; 73pp; English.
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        2001-016048/02
        WPI; 2001-016048/
N-PSDB; AAA54499.
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                                                                                                                                                                                             SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
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                                                                                     GIYSSKPSEVNIAQNNDIIXNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                               SYTNDKILLLYFUKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                            NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                        WKISLNYNKIIWTLQDTAGNNOKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
                                                   1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                Length 431;
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                                   Indels
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                 100.0%; Score 2288; DB 2; 100.0%; Pred. No. 2.6e-167;
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                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  AAB04103 standard; protein; 432 AA
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99US-0133866P.
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                                   Conservative
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Clostridium botulinum.
                          Similarity
 Sequence 431 AA;
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12-MAY-1999;
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12-MAY-1999;
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                                    Matches 431;
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Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a cond then posttranslationally nicked, forming a dichain consisting of a clisulfide bond. Wacleic acide encoding the carboxy-terminal (HC) or amino terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acide are expressible in a recombinant companisms such as Escherichia colio are expressible in a recombinant colio acide are advantageous since it eliminates the need coulure large quantities of hazardous toxin-producing bacterium.

Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acide can be derived from
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New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine against botulism.
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100.0%; Score 2288; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 431; Conservative 0; Mismatches 0;
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Silman N;
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07-APR-2000; 2000GB-00008658.
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Clostridium botulinum.
Chimeric.
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01-NOV-2001
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                              Botulism; toxin; neurotoxin; heavy chain; recombinant expression;
                                              recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
Botulism toxin heavy chain C-terminal sequence (serotype F)
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                                                                                                                                                                                                                                                                                                                                                                              Lapenotiere
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; Pred. No. 2.6e-167;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                           Byrne MP, Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 9b; 73pp; English.
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Best Local Similarity 100.0%;
Matches 431; Conservative 0;
                                                                                                                                                                                                                                         99US-0133866P.
99US-0133867P.
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                                                                                                                                                                                                                                                                                                                  99US-0146192P
                                                                                        Synthetic.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-016048/02.
N-PSDB; AAA54490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                against botulism.
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                                                                                                                                   WO200067700-A2
                                                                                                                                                                                              12-MAY-2000;
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12-MAY-1999
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12-MAY-1999
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carbox terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell, where the translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial cell, where the translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the transment of a disease state associated with neuronal useful for the polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for delivering therapeutic substances to neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                       360
                                                                           301
                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                       NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified clostridial heavy chain fragment #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE07894 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 44; 50pp; English
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                           GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spaem; (OOD); bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; translocation domain; HN domain; DipT; HC; botulinum type F neurotoxin; binding domain; BONT/F.
                                                                                                                                                                                                                         SYTNDKILILLYFUKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
(BoNT/F) with translocation domain of diphtheria neurotoxin. (Updated 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                            1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILKDFWGNYLLYNKRYYLLNLLRIDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                      Gaps
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                                                                                                            Length 645;
                                                                                                                                                    Indels
                                                                                                          100.0%; Score 2288; DB 4; 100.0%; Pred. No. 4.3e-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium diphtheriae.
Clostridium botulinum.
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                                                                                                                                                      Matches 431; Conservative
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                                                                                                      Query Match
Best Local Similarity
                                                                  Sequence 645 AA;
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; promoting or inhibiting and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory compliance from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular crafficking, for modulating expression of cell-surface markers and for trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and the second comprising corpusatorerium diphtheriae diphtheria toxin translocation comming in this sequence is used in the exemplification of the invention. Compusion This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
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                                                                                                      Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 2288; DB 6;
; Pred. No. 4.3e-167;
0; Mismatches 0;
                                                                                                                                                                                                                            Example 12; Page 57-60; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Matches 431; Conservative
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  Shone CC;
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Best Local Similarity
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Sutton JM,
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating prion disease, Alzheimer' disease and wide range of disorders including muscle spages such as blephorospasm, toticolis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HN domain), botulinum type F neurotoxin binding domain (BoNT/F-Hc) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion constru
                                                                                                                                                          Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzhelmer' disease; hypersecretion disorder; muscle spaem; OOD9; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain;
                                                                                                                      BoNT/F-Hc-DipT HN domain-thrombin linker fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; Page 60-63; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY.
  AAE35693 standard; protein; 657 AA.
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100.0%;
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                                                                                                                                                                                                                                                                                                                  Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                            botulinum type F neurotoxin
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                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutton JM, Shone CC;
                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-167247/16.
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                                                                                   17-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                    Chimeric.
                                         AAE35693
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Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain; Apoptosis, therapy, inflammatory mediator, intracellular trafficking, infection, Prion disease, Alzheimer' disease, hypersecretion disorder; SILKDFWGNYLLYNKRYYLLINLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP BONT/F-Hc-DipT HN domain-factor Xa linker fusion construct. (MICR-) MICROBIOLOGICAL RES AUTHORITY Š AAE35694 standard; protein; 657 Page 63-65; 130pp; 21-MAY-2002; 2002WO-GB002384 24-MAY-2001; 2001GB-00012687 Corynebacterium diphtheriae. Clostridium botulinum. botulinum type F neurotoxin (first entry) 431 657 Shone CC; PISKEHGWQEN FISKEHGWQEN WPI; 2003-167247/16. WO200296467-A2. Clostridium b Unidentified. Example 12; 05-DEC-2002. 17-JUN-2003 Sutton JM, 181 241 467 527 361 421 647 301 Chimeric AAE35694 RESULT 원 셤 g ò 셤 ò g 8 요 ò ò

646

360 586 420

240 466 300 526

406

287 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG

WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for treatment selected from promoting or inhibiting survival of cells;

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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 227 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF

286

GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBYTIIDCIRNNNSG 120

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0; Mismatches

4.5e-167;

Score 2288; DB 6; Pred. No. 4.5e-167;

Length 657;

The present sequence is a fusion construct

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preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders inhibiting secretion disorders such as blephorospasm, torticols and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comparising Corymebacterium diphtheriae diphtheria toxin translocation domain (DipT-HN domain), botulinum type F neurotoxin binding domain (BobT-Ho from Clostridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention
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(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Shone CC, Sutton JM, WPI; 2001-514643/56

04-DEC-2000; 2000WO-GB004644 02-DEC-1999; 99GB-00028530 07-APR-2000; 2000GB-00008658

WO200158936-A2 16-AUG-2001

Synthetic. Chimeric.

## Sequence 657 AA;

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                                                                                                                                              GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 346
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                                                                                                                        GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                     WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
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                                                                                                                                                                                                                    WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 406
                                                                                                                                                                                                                                                                               NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 466
                                                                                                                                                                                                                                                                                                                                                                                                                                          NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                                                                                                                                                                                                                                                                                 SILKDEWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                            SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                            1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                   NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                               Gaps
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100.0%; Score 2288; DB 6; Length 657; 100.0%; Pred. No. 4.5e-167;
                               0; Indels
                             0; Mismatches
              Best Local Similarity 100.
Matches 431; Conservative
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### AAE07893 standard; protein; 685 AA. 01-NOV-2001 AAE07893; RESULT 8

(first entry)

Modified clostridial heavy chain-superoxide dismutase conjugate #5.

Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; botulinum neurotoxin type F; BONT/F.

Geobacillus stearothermophilus Influenza virus. Clostridium botulinum.

The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell, which comprises a binding domain capent into the neuronal cell, where the translocation domain is not a terminal half of HC, designated as HN), that translocates the therapeutic capent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are casful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the conjuding neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa, translocation peptide from influence virus and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F) New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells. Example 9; Page 43; 50pp; English Sequence 685 AA; 

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ö 120 240 300 EVIIRKAGSTDISNTDNFVPRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 614 314 374 121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180 434 494 554 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360 315 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP SYTNDKILLLYFUKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTURNQF 255 SYTNDKILILYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 181 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV Gaps . 0 Length 685; Indels Score 2288; DB 4; Pred. No. 4.7e-167; 0; Mismatches 0; 100.0%; Query Match 100. Best Local Similarity 100. Matches 431; Conservative 375 н 61 435 241 495 555 301

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                  615 NSLGQIIVWDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 674
                                                                                                                                                                                                                                                                                                               Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                Modified clostridial heavy chain-superoxide dismutase conjugate #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from diphtheria neurotoxin and a neuronal
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                                                                                                                                                                                AAE07890 standard; protein; 862 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                 Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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                                                                 FISKEHGWOEN
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100.0%; Score 2288;

Query Match

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                                                                                                                                                                                                                          792 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                                                                                                                                                       121 WKISLNYNKIIWTLQDTAGNNOKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
                                                                                                                                                                                                                                                                241 SILKDFWGNYLLYNKRYYLLMLLRTDKSITQNSNFLMINQQRGVYQKPNIFSNTRLYTGV
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                                                                                                                                                                                                            181 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified clostridial heavy chain-superoxide dismutase conjugate #4.
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         Pred. No. 6.3e-167;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE07892 standard; protein; 887 AA.
100.0%; Pre-
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Clostridium botulinum.
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            Best Local Similarity 100.
Matches 431; Conservative
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the invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises a mitochondrial leader sequence from human Mn-simple comprises (MNSOD) from Bacillus stearchermophilus, linker that can be cleaved by thrombin, translocation domain from diphtheria neurotoxin and a neuronal cell-specific binding domain from conjugate. New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells. 42; 50pp; English 

Gaps ô 100.0%; Score 2288; DB 4; Length 887; 100.0%; Pred. No. 6.5e-167; ative 0; Mismatches 0; Indels 0 Query Match
Best Local Similarity 100.
Matches 431; Conservative Sequence 887 AA;

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SYTNDKILLLYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 516 636 240 756 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 696 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP SILKDFWGNYLLYNKRYYLLNLLRIDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 457 181 637 121 517 241 61 g 셤 a ð 요 ò g ઠે ठ

EVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRISNSN 360 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 697 757 301 ઠ g NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420

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FISKEHGWOEN

877

AAE35713 standard, protein; RESULT 11 AAE35713 H

979 AA. (first entry) 17-JUN-2003 AAE35713;

Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. BONT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spaem; CODP; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; HC; binding domain; botulinum type F neurotoxin; targetted effector protien; YopT. Example 12; Page 110-114; 130pp; English. (MICR-) MICROBIOLOGICAL RES AUTHORITY. 24-MAY-2001; 2001GB-00012687 21-MAY-2002; 2002WO-GB002384 Corynebacterium diphtheriae. Clostridium botulinum. Shone CC; WPI; 2003-167247/16 Yersinia pestis. WO200296467-A2 Unidentified. 05-DEC-2002 Sutton JM, Chimeric 

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a targets the effector protein to a tradect call. The management of composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells. Dreworting and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection, and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking for modulating expression of cell-surface markers and for thibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer disease and wide range of disorders including muscle spasms such as blephorospasm, torticals and control of the control o hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HM domain). Notulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and factor Xa linker peptide and Yersinia pestis targetted effector protien YopT. This sequence is used in the exemplification of the invention

608 09 SYINDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYTYSTNRNQF 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF Gaps ö Length 979; Indels ; Score 2288; DB 6; ; Pred. No. 7.4e-167; 0; Mismatches 0; 100.0%; Matches 431; Conservative Query Match Best Local Similarity 549

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Sequence 979 AA;

WKISLNYNKIIWTLODTAGNNOKLVFNYTOMISISDYINKWIFVTITNNRLGNSRIYING 180 121

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WO200028041-A1
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Matches 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                 SILKDFWGNYLLYNKRYYLLNLTRIDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 848
                                                                                                                                                                                                909 NSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 968
                                                                                                                               EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                                                                     EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 908
                                                                                                                                                                                 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
669 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 728
                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BoNT/F.
                                         NIIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                            NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                              SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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                                                                                                                                                                                                                                                                                                                                 AAE07901 standard; protein; 1032 AA.
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                                                                                                                                                                                                                                                                                                                                                                is C. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BoNT/F) binding domain used in the exemplification of the invention
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                                                                                                                                                 Length 1032;
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                                                                                                                                                                                             Indels
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                                                                                                                                            100.0%; Score 2288; DB 4;
100.0%; Pred. No. 7.9e-167;
                                                                                                                                                                                                  0; Mismatches
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Clostridium botulinum.
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                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                          The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases
                                                                                                                  cleavable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                        Novel composition, comprising superoxide dismutase linked by a clear linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2288; DB 3;
100.0%; Pred. No. 8.2e-167;
tive 0; Mismatches 0;
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Silman
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Hallis B,
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Sutton JM,
                                                         WPI; 2000-376553/32
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The present sequence represents a construct of the invention, comprising a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SOD). a Bacillus stearothermophilus Mn-SOD, a linker that can be cleaved by thrombin and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               654 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIFTLYSDEPDP
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              Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1084;
neuronal cell targeting component; NCTC; neuronal disease;
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100.0%; Pred. No. 8.4e-167;
tive 0; Mismatches 0;
                oxidative stress; ischemic stroke; trauma; P:
Huntington's disease; motor neurone disease;
botulinum neurotoxin serotype F.
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                                                                                                                                                                                                                                                                                                              (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 57-60; 65pp; English
                                                                                                    Homo sapiens.
Geobacillus stearothermophilus.
Clostridium botulinum.
                                                                                                                                                                                                                                           99WO-GB003699
                                                                                                                                                                                                                                                                             98GB-00024282
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Best Local Similarity 100.
Matches 431; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motor neurone diseases
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN commain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum
                    1014 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYNNNIRKNTSSNGCFWS 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
NSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                                                                                                                                                                                                                                                                                       Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                      C2 translocation domain with BONT/F-binding domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                              AAE07900 standard; protein; 1092 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2000; 2000WO-GB004644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1999; 99GB-00028530
07-APR-2000; 2000GB-00008658
                                                                                                                                                                                                                                                                      (first entry)
                                                                                           421 FISKEHGWQEN 431
                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sutton JM,
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                                                                                                                                                                                                                                                                                                      C. botulinum
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Length .1092;

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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF

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Query Match 100.0%; Score 2288; DB 4; Best Local Similarity 100.0%; Pred. No. 8.5e-167; Matches 431; Conservative 0; Mismatches 0;

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1081
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                                                                                                                                                       SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
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                                                                                                                                                                                                                   EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 781
                                 180
                                                   NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
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                                                                                                            902 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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                                                                                                                                                                                                                                                                                NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                                  WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
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Job time : 209.5 secs
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# GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

model using protein search, protein March Run on:

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(without alignments)
1151.928 Million cell updates/sec

Title: Perfect score:

US-08-981-087B-1 2288 1 SYTNDKILILYFNKLYKKIK.....TSSNGCFWSFISKEHGWQEN

431

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 283416 segs, 96216763 Searched: of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

R\_80:\* pir1:\* pir2:\* pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	1833	80.1	1274	2	140813	neurotoxin type F
~	1827	79.9	1268	7	S33411	botulinum neurotox
e	1457.5	63.7	1252	~	S21178	botulinum neurotox
4	1426	62.3	1251	7	JH0256	botulinum neurotox
'n	1120.5	49.0	1296	Н	BTCLAB	bontoxilysin (EC 3
9	1092.5	47.7	1296	~	I40645	botulinum neurotox
7	816	35.7	366	~	S48110	neurotoxin type F
80	781	34.1	1291	7	140631	r
σ	769	33.6	1291		A48940	bontoxilysin (EC 3
10	736.5	32.2	1297	~	839791	neurotoxin - Clost
11	645.5	28.2	369	~	S48109	neurotoxin type F
12	590.5	25.8	367	~	S48106.	neurotoxin type E
13	580.5	25.4	1276	7	S11455	botulinum neurotox
14	553	24.2	1315	-	BICLIN	tentoxilysin (EC 3
15	546	23.9	1291	N	A49777	
16	546	23.9	1291	~	S46431	botulinum neurotox
17	508	22.2	1285	~	S70582	botulinum neurotox
18	267	11.7	1162	7	140817	botulinum toxin no
19	260	11.4	1162	7	A47708	progenitor toxin n
20	259	11.3	1193	7	868218	botulinum neurotox
21	244	10.7	1193	••	JC4901	nontoxic-nonhemagg
22	225.5		1196	~	JQ1467	toxin, nontoxic co
23	225.5	9.6	1196	•	S46430	botulinum neurotox
24	208.5	9.		N	I40644	botulinum neurotox
25	201			~	A53878 ·	type E neurotoxin
26	190	æ	1844	~	D71612	
27	172.5	7.5	2136	N	A05037	
28	169	7.4	4688	~	F82885	prot
29	165.5	7.2	096	~	S72284	DNA-directed RNA p

hypothetical prote	DNA-directed KNA p	hypothetical prote	hypothetical prote	hypothetical prote	DNA-directed RNA p	hypothetical prote	ATP-dependent Clp	hypothetical prote	protein with 5'-3'	toxin-like outer m					
T18501	A45597	D71618	T18440	T18469	RNZQBF	A71661	B71612	B71605	T18460	B90590	E71616 .	872278	C64474	A71621	B64596
~	~	~	N	~	-	~	~	~	~	7	~	~	~	~	7
3394	2339	1436	4550	786	1024	588	3973	807	836	640	1247	765	2894	1188	1943
7.2	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.8
164	163	162.5	162.5	161.5	161.5	160	160	159.5	159.5	159	158	157.5	157.5	157	156.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

-	
SULT	10813

neurotoxin type F - Clostridium botulinum C;Species: Clostridium botulinum

16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

A;Accession: 140813
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
B;Rcdambell: K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Accession: 548108
A;Status: preliminary; translation not shown

A;Molecule type: DNA \*\* Residues: 634-1002 <CAM>\*\* Residues: 634-1002 <CAM>\*\* A;Residues: 634-1002 <CAM>\*\* A;Cross-references: UNIPARC: UPI000016EA7B; EMBL: X70816; NID: 9407788; PIDN: CAAS0147.1; PI C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

8; Gaps Length 1274; 40, Indels Query Match 80.1%; Score 1833; DB 2; Best Local Similarity 81.3%; Pred. No. 8.4e-98; Matches 352; Conservative 33; Mismatches 40;

906 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIXSTNRNQF g ò

120 996 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNIANBYTIIDCIRNNNSG Š 유

WKISLNYNK---IIWILQDIAGNNQKLVPNYTQMISISDYINKWIFVTITNNRLGNSRIY 177 121 ઠે

178 INGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDE 셤 ઠ

1027 INGNLIVEKSISNLGDIHVSDNILFKIVGCDDETYVGIRYFKVFNTELDKTEITLYSNE a

1145 셤

PDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLY

238

ò

TGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTS 357 298

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A; Reduces: 616-982 < CAM>
A; Cross-references: UNIPARC:UPI0000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; P. A; Cross-references: UNIPARC:UPI0000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; P. A; Cross-references: UNIPARC:UPI0000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; P. A; Cross-reference bequence was submitted to the EMBL Data Library, January 1993 A; Pittle: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum typ: A; Reference number: JH0255; MUD:92181428; PMID:1543481 A; Reference number: JH0257 MID:92181428; PMID:1543481 A; Reference number: JH0257 A; Reference not shown A; Redecule type: DNA A; Residues: 1-176, R, 178-197, C', 199-339, R', 341-772, 'I', 774-962, 'FE', 965-966, 'R', 968-: A; Cross-references: UNIPARC:UPI000016EA7F; EMBL:X62089; NID:940393; PIDN:CAA43999.1; PII A; Experimental source: strain Beluga R; Biio: Chem: 265, 9153-9158, 1990 A; Title: The complete sequence of botulinum neurotoxin type A and comparison with other A; Reference number: A35294; MUD:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Residues: 1-176, 'R', '18-25 < BIN>
A;Residues: 1-176, 'R', '18-25 < BIN>
A;Experimental source: strain Beluga
A;Experimental source: strain Beluga
B;Gimenez, J.A.; DasGupta, B.R.
Biochimia 72, 213-217, 1990
A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the s:
A;Reference number: A60027; MUID:90344918; PMID:2116911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: strain Beluga
A, Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin
C, Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu
C, Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
                                                                    neurotoxi
                                                                                                                                                                                                    EMBL: X62683;
                                                                                                                                                                                                                                                                                 neurotoxin gene and specific
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     R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P. Bur. J. Biochem. 204, 657-667, 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E
A;Reference number: S21178; MUID:92174922; PMID:1541280
                                                                                                                                     A, Molecule type: DNA
A, Residues: 1-1252 < WHES
A, Residues: 1-1252 < WHES
A, Cross-references: UNIPROT: Q00496; UNIPROT: Q45862; UNIPARC: UPI00000010A3; EMB
A, Cross-references: UNIPROT: Q00496; UNIPROT: Q45862; UNIPARC: UPI00000010A3; EMB
R, Campbell, K.D.; Collins, M.D.; Bast, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A, Title: Gene probes for identification of the botulinal neurotoxin gene and s
A, Reference number: S48103; MUID: 94013372; PMID: 8408542
A, Accession: S48107
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A60027
Modecule type: protein
A;Residues: 420-427
A;Cross-references: UNIPARC:UP10000176710
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                                                                                                                 A; Accession: S21178
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                                                                                                                                                                                                                                                                                                                                               Doculinum neurotoxin type F - Clostridium barati

botulinum neurotoxin type F - Clostridium barati

botulinum neurotoxin type F - Clostridium barati

c;Species Clostridium barati

c;Accession: 833411, 831860

c;Accession: 833411, 831860

R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.

FERS Microbiol. Lett. 108, 175-182, 1993

A;Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin

A;Reference number: 833411

A;Accession: 833411

A;Residues: DNA

A;Residues: DNA

A;Residues: 1-1268 <THO>

A;Residues: 1-1268 <THO>

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin
                                                                                                                    NINDSLGQIIVMDSIGNNCTWNFQNNNGSNIGLLGFHSNNLVASSWYYNNIRRNTSSNGC 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960 KISLNYNNIIWTLQDTTGNNQKLVFNYTQMIDISDYINKWTFVTITNNRLGHSKLYINGN 1019
ö
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botulinum neurotoxin type E precursor - Clostridium botulinum
C;Species: Clostridium botulinum c;Species: Clostridium botulinum c;Cjate: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 31-Dec-2004
C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYSSRLSEVNITQNNTIIYNSRYQNPSVSFWVRIPKYNNLKXLLNNEYTIINCMRNNNSGW
                                                                                     NSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGC
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                                                                                                                                                                                                                                              FWSSISKENGWKE 1274
                                                                                                                                                                                           FWSFISKEHGWQE 430
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38; Conservative
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Matches 338;
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A, Residues: 1-1296 (BIN)
A, Residues: 1-1296 (BIN)
A, Cross-references: UNIPROT: P10845; UNIPARC: UP10000001386; GB:M30196; NID: g144864; PIDN: A, Experimental source: strain 62A, subtype A
R, Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T. Bur. J. Biochem. 189, 73-81, 1990
Bur. J. Biochem. 189, 73-81, 1990
A, Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin A, Reference number: S09492; MUID: 90235864; PMID: 2185020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1,'O',3-26,'V',28-1296 <THO>
A;Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: NCTC 2916
R; Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A; Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A; Reference number: .867988; MUID: 96096783; PMID: 8521962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jórosa-references: UNIPARC:UPI0000173655; EMBL:D67030; DDBJ:D50421; NID:g2160224; Betley, M.J.; Somers, E.; DasGupta, B.R. dochem. Bophys. Res. Commun. 162, 1388-1395, 1989; Inchem. Blophys. Res. Commun. 162, 1388-1395, 1989; Inchem. Characterization of botulinum type A neurotoxin gene: delineation of the N-term; Reference number: A33401; MUID:89350959; PMID:2669749
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A,Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after ex-
R,DasGupta, B.R., Deklewa, M.L.
Biochimie 72, 661-664, 1990
A,Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and aro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denicoxilygin (BC 3.4.24.69) A precursor - Clostridium botulinum
NyAlternate names: botulinum neurotoxin type A
Cispecies: Clostridium botulinum
Cispecies: Clostridium botulinum
Cipaces 31-Mar-1993 #eequence revision 31-Mar-1993 #text change 09-Jul-2004
Cipaces 31-Mar-1993 #eequence revision 31-Mar-1993 #text change 09-Jul-2004
Cipaces 31-Mar-1993 #eequence revision 31-Mar-1993 #text change 09-Jul-2004
Cipaces 31-Mar-1993 #eequence 0. Fervert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
Airlie The complete sequence of botulinum neurotoxin type A and comparison with Airlie number: A35294; MUID: 90264400; PMID:2160960
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                                                                                                                                              GVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKIIKLIR
240 PSILKDFWGNYLLYNKRYYLLMLLRTDKSITQNS-NFLNINQQRGVYQKPNIFSNTRLYT
                                                                                                                                                                                                                                                                                                 TSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSN
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A;Residues: 867-880;1148-1217,'Y',1219 <GIM>
A;Cross-references: UNIPARC:UPI00000BBB24; UNIPARC:UPI0000173656
                                           A;Cross-rererence.
R;Gimenez, J.A.; DasGupta, B.R.
J. Protein Chem. 12, 351-363, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCFWSFISKEHGWOE 430
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Residues: 1-12 <FUJ>
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A; Residues: 1-35 <BET>
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C;Species: Clostridium butyricum
C;Species: Clostridium butyricum
C;Species: Clostridium butyricum
C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
C;Accession: JH0256; S16145
R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem: Biophys. Res. Commun. 183, 107-113, 1992
A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type
A;Reference number: JH0256; MUID:92181428; PMID:1543481
A;Reference number: JH0256; MUID:92181428; PMID:1543481
A;Reference number: JNRROR:12310995; UNIPARC:UPID00017670D; EMBL:X62088; NID:g40379
A;Residues: 1-27, E', 29-1251 cPOU>
A;Residues: 1-27, E', 29-1251 cPOU>
A;Residues: 1-27, E', 29-1251 cPOU>
A;Residues: 1-37, E', 29-1251 cPOU>
A;Reperimental source: strains ATCC 43181 and ATCC 43755
R;Pujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N.
J, Gen. Microbiol. 137, 519-525, 1991
A;Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxi
A;Accession: S16145; MUID:91237316; PMID:2033376
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A;Molecule type: DNA
A;Molecu
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                                                                                                                                                                                                                                                                                                 GWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYIN 179
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               1009 GNLIDQKSILNLGNIHVSDNILFKIVNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPN 1068
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                                                                                       240 PSILKDFWGNYLLYNKRYYLLNLLRTDKSI-TQNSNFLNINQQRGVYQKPNIFSNTRLYT 298
                                                                                                                                                                                                                                         GVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKIIKLIR 355
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                                                                                                                              GCFWSFISKEHGWQE 430
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Best Local Similarity
Matches 273; Conserv
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A,Accession: 146645
A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-126 cAREX
A,Cross-references: UNIPROT:Q45894; UNIPARC:UPI000016EA88; EMBL:X73423; NID:g507070; PIC
C,Superfamily: tetanus toxin
C,Keywords: neurotoxin
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                                              of Clostridium botulinum type
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A;Residues: 1-366 <CAM>
A;Cross-references: UNIPROT:Q57236; UNIPARC:UPI000016EA7C; EMBL:X70821; NID:g407792;
C;Superfamily: Letanus toxin
C;Keywords: neurotoxin
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S48110
A;Pitle: Gene probes for identification of the botulinal neurotoxin gene and the A;Pitle: Gene probes for identification of the botulinal neurotoxin gene and the A;Pitle: S48103 #UID:94013372; PMID:8408542
A;Accession: S48110
A;Status: preliminary; translation not shown
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Rightlems, A.; East, A.K.; Lawson, P.A.; Collins, M.D. Res. Microbiol. 144, 547-556, 1993
A;Title: Sequence of the gene coding for the neurotoxin A;Reference number: 140645; MUID:94143603; PMID:8310180
                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                      47.7%; Score 1092.5; DB 2;
48.6%; Pred. No. 3.2e-55;
tive 76; Mismatches 133;
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Best Local Similarity 48.6$
Matches 216; Conservative
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Best Local Simi
Matches 153;
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A; Residues: 2-47 cDAS2-
A; Cross-references: UNIPARC:UDI0000173659
A; Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A; Reference number: A49708; MUID:94124495; PMID:8294407
A; Contents: annotation
C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap C; Genetics:
A; Gene: atx; botA
C; Function:
A; Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C; Superfamily: tetanus toxin
C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot C; Superfamily: tetanus toxin
C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot C; Superfamily: tetanus toxin
C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot C; Superfamily: tetanus forcitylysin A heavy chain #status experimental <HVX>
F; 223, 227/Rainding site: zinc (His) #status predicted
F; 224/Active site: Glu #status predicted
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botulinum neurotoxin type A - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40645
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    A;Reference number: A60025; MUID:91120847; PMID:2126206
A;Accession: A60025
A;Accession: Drotein
A;Accession: Drotein
A;Residues: 2-6;445-453, 7X', 455-457 <DASI>
A;Cross-references: UNIPARC:UP10000173657; UNIPARC:UP10000173658
B;Cross-references: UNIPARC:UP10000173658
B;Cross-references: UNIPARC:UP10000173658
A;Trile: Partial sequence of the light chain of botulinum neurotoxin type
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49.0%; Score 1120.5; DB 1; Length
Best Local Similarity 49.4%; Pred. No. 7.8e-57;
Matches 219; Conservative 78; Mismatches 127; Indels
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bontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum
N.Alternate names: botulinum neurotoxin type B (BoNT/B)
C;Species: Clostridium botulinum
C;Species: J-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48940; S48105; S21575; A42811; S07155; S08562; S07128; S08574
R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. 58, 2345-2354, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the typ
A;Reference number: A48940; MUID:92384550; PMID:1514783
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A; Cross-references: UNIPROT: P10844; UNIPARC: UPI000016EA76; GB:M81186; NID:g144734; PIDN: A; Cross-references: UNIPROT: P10844; UNIPARC: UPI000016EA76; GB:M81186; NID:g144734; PIDN: A; Experimental source: type B, Danish A; Note: sequence extracted to NCBI Dackbone (NCBIN:112080, NCBIP:112081); this publica R; Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A; Tritle: Gene probes for identification of the botulinal neurotoxin gene and specific id A; Reference number: S48103; MUID:94013372; PMID:8408542
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A;Residues: 614-994 < CAM>
A;Residues: 614-994 < CAM>
A;Residues: 614-994 < CAM>
A;Residues: 614-994 < CAM>
A;Xrosareferences: UNIPARC:UPI000016EA7A; EMBL:X70817; NID:g407782; PIDN:CAA50148.1; JA;Xrosareferences: UNIPARC:UPI00016EA7A; EMBL:X70817; NID:g407782; PIDN:CAA50148.1; JA;Szabo, E.A.; Pemberton, J.M.; Dosmarchelier, P.M.
R;Szabo, E.A.; Pemberton, J.M.; Dosmarchelier, P.M.
Submitted to the EMBL Data Library, April 1992
A;Description: Partial amino acid sequence of botulinum neurotoxin type B and comparis: A;Reference number: S21575
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QSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLVKDSSVGEILIRSKYNQNSNYINYR 1137
                                                                                                                                                                             TONSNFLNIN 279
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                                                                                                                                  QQRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLY
                                                                                                                                                                                                                                                                       340 ADISIAKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH
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                                                                                                                                                                                                                                                                                                                                                                                                                    ---SNNLVASSWYYNNI-RKNTSSN-GCFWSFISKEHGWQE 430
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Note: sequence extracted from NCBI backbone (NCBIP:109365)
DasGupta, B.R.; Datta, A.
iochimie 70, 811-817, 1988
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A;Residues: 2-29,'M', 31-45 <DAS>
A;Cross-references: UNIPARC:UP10000173650
A;Accession: 808562
   237 EPDPSILKDFWGNYLLYNKRYYLLNL--
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Cispeciae: Clostridium botulinum mercervision 12-Mag-1996 #text_change 09-Jul-2004
Cispeciae: Clostridium cervision 13-Mag-1994
Ayritle: Mucleocide sequence of the gene coding for non-proteolytic Clostridium botulinum A;Reference number: 140631; MUID:94122659; PMID:7764370
A;Retus: perellininary; translated from GB/BMBL/DDBJ
A;Retus: perellininary; translated from GB/BMBL/DDBJ
A;Retus: perellininary; translated from GB/BMBL/DDBJ
A;Roces-references: UNIPROT:008077; UNIPARC:UP100000BDC86; EMBL:X71343; NID:9296148; PIIC
R; campbell, K.D.; Collins, M.D.; East, A.K.
A;Rocession: S48103
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
A;Retus: perellininary; nucleic acid sequence not shown; translation not shown
A;Rocession: S48103
A;Accession: S48104
A;Accession: Colliminary
A;Accession: S48104
A;Accession: S48104
A;Accession: Bytudian accession: NulPakc:UP1000000BPA6E; EMBL:X70819; NID:9407789; PIDN:CAA50150.1; PI
A;Accession: S48104
A;Accession: Bytudian accession: NulPakc:UP1000000BPA6E; Exatins Product: Doculinum neurotoxin type B light chain #satus predicted <IGHT>
C;Comment: Botulinum neurotoxin type B light chain #satus predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 INGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSD 236
                                                                           GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG 120
                                                                                                                   214 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-proteolytic botulinum neurotoxin type B precursor - Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYTNDKILILYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.1%; Score 781; DB 2;
llarity 37.0%; Pred. No. 2.5e-37;
Conservative 90; Mismatches 146;
                                                                                                                                                                                                                 121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMIS 153
                                                                                                                                                                                                                                                         334 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMIS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local Si
Matches 174
                                                                               61
                                                                                                                                                274
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C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S39791
K;Campbell, K.; Collins, M.D.; East, A.K.
Biochim. Biophys. Acta 1216, 487-491, 1993
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium A;Reference number: S39791; MUID:94092745; PMID:8268233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specific
                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 11297 <CAM>
A;Cross-references: UNIPARC:UPI0000176706; EMBL:X74162; NID:g441275; PIDN:CAA52275.1;
C;Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P30996; UNIPARC:UPI000016EA7B; EMBL:X70820; NID:g407790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTOLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDYGYVWD 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 PDPSILKDFWGNYLLYNKRYYLLN-----LLRTDKSITQNSNFLNINQQRGVYQKPN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotoxin type F - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Datesino S;Collins, M.D.; East, A.K.
J. Clin Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and A;Reference number: S48103; MuID:94013372; PMID:8408542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 IFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVD-RDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN
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A;Residues: 1-369 <CAM>
1243 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 736.5; DB 2;
; Pred. No. 9.2e-35;
76; Mismatches 179;
                                                                                                                           neurotoxin - Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.7%;
Matches 164; Conservative 78
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: ccc....
C; Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                     A,Accession: S39791
A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: $27125; MUID:93063293; PMID:1331807
A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
C;Genetics:
A;Genee: bott/b
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ature 359, 832-835, 1992
Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteoly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              m.
                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: 808574
Status: pretaininary
Nolecule type: protein
Nolecule type: protein
Residues: 442-459 <8CH3>
Cross-references: UNIPARC:UPI0000173652
Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, Schiavo, G.; Banfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, Schiavo, G.; Banfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, Schiavo, G.; Banfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, Bature 359, 832-835, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2 C, Superfamily: tetanus toxin C; Superfamily: tetanus toxin C; Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc E; Z44, Product: bontoxilysin B light chain #status experimental <LGHT> F; 442-1291/Product: bontoxilysin B heavy chain #status experimental <HVY> F; 230, 234/Binding site: zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRD 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1183 YKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHR 1242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 QRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIFTLYSDE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISIAKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH- 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1291;
                                                                                             Arch. Biochem. Biophys. 238, 544-548, 1985.
A;Title: Partial amino acid sequences of botulinum neurotoxins
A;Reference number: S07128; MUID:85197963; PMID:3888113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 769; DB 1; Length 12 llarity 36.0%; Pred. No. 1.2e-36; Conservative 88; Mismatches 152; Indels
                                                                                В.К
       A,Molecule type: protein
A,Residues: 442-463, "7',465-467 <DA2>
A,Tobs-dreferences: UNIPARC:UPI0000173650
R,Schmidt, J.J.; Sathyamoorthy, V.; DasGupta,
                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UP10000173652
A;Accession: S08573
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 2-17 <SCH2>
A;Cross-references: UNIPARC:UP10000173652
                                                                                                                                                                             A;Accession: S07128
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-16 <SCH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
169; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 169
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tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
N;Alternate names: tetanus neurotoxin
C;Space: Clostridium tetani
C;Date: 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
EMBO J. 5, Z495-2502, 1986
A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botu
A;Reference number: A25689; MUID:87053814; PMID:3536478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-1315 cEIS>
A,Gross-references: UNIPROT: P04958; UNIPARC: UPI000003617E; GB:X04436; NID:g40769; PIDN:C
R,Fairweather, N.F.; Lyness, V.A.
R,Fairweather, N.F.; Lyness, V.A.
A,Title: The complete nucleotide sequence of tetanus toxin.
A,Reference number: A25757; MUID:87040747; PMID:3774547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reddues: 1-1315 cRAI>
A;Reddues: 1-1315 cRAI>
A;Cross-references: UNIPRAC:UPI00003617E; GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g
A;Cross-references: UNIPRAC:UPI00003617E; GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g
A;Experimental source: strain CN3911
B;Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986
J. Bacteriol. 165, 21-27, 1986
J. A;Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in I
A;Reference number: A25194; MUID:86085672; PMID:3510187
A;Accession: A25194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPARC: UPI0000156CFA; GB: M12739; NID: g144920; PIDN: AAA23282.1; PID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1082 RNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLVL-----VQYPD---RSKLYTG 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TQGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVSKNKYCSQ 1219
                                                                                                                                                                                                                                                                                                                                                                             121 WKISLAYYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 NLIDEKSISNLGDIHVSDNILFKI-VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 VEVIIR----KNGSTDISNTDNFVRK---NDLAYINVVDRDVEYRLYADISIAKPEKIIK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 LIRTSNSNNSLGQIIVMDSIGNNCTMNF----QNNNGGNIGLLGFHSNNLVASSWY--- 404
                                                                                                                                                                                                                                       61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 PSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQORGVYQKPNIFSNTRLYTG
                                                                                                                                SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                      93;
                                                                                 Indels
                                                                                    88; Mismatches 156;
                                   Score 580.5; DB 2
Pred. No. 8.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 -YNNIRKNTS------
                                   25.4%;
                                                                                    Conservative
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A; Residues: 743-1315 < FA2>
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A;Molecule type: protein
A;Residues: 865-894 <FA3>
                                Query Match
Best Local Similarity
Matches 140; Conserv
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C;Species: Clostridium botulinum
C;Saccession: S48106
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
A;Reference number: S48103; MUD:94013372; PMID:8408542
A;Stecusion: S48106
A;Stetus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-367 < CAM>A;Residues: 1-367 < CAM>A;Residues: 1-367 < CAM>A;Residues: Loson: Csample sequence was submitted to the EMBL Data Library, January 1993
C;Superfamily: tetanus toxin
C;Reywords: neurotoxin
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R. Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, S.; Kriegls
R. Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, S.; Kriegls
R. Binz, T.; Kurazono, H.; 556, 1990
A; Title: Nuclectide sequence of the gene encoding Clostridium botulinum neurotoxin type
A; Reference number: S11455, MUID: 91016853; PMID: 2216736
A; Accession: S11455
A; Status: preliminary; translation not shown
A; Residues: preliminary;
A; Residues: 1-1776 csIIN
A; Crosss-references: UNIPROY: P19321; UNIPARC: UPI0000126B83; EMBL: X54254; NID: g40395; PIDN
C; Superfamily: tetanus toxin
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 C;Superfamily: tetanus toxin
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                                                                                                                                                                                                                                                                                                   GIYSSKPSEVNIAONNDIIYNGRYONFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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botulinum neurotoxin type D - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                          214 SYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQP
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                                                                                    Length 369;
                                                                                                                                           14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.8%; Score 590.5; DB 2; 71.8%; Pred. No. 4.8e-27; ive 25; Mismatches 16;
                                                                                         DB 2;
                                                                                    ; Score 645.5; DB 2
; Pred. No. 3.4e-30;
17; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                      WKISLNYNK---IIWTLQDTAGNNOKLVFNYTQM 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 GWKVSLNHNEIIWTLQDNAGINQKLAFNY 362
                                                                                    Query Match 28.2%;
Best Local Similarity 77.9%;
Matches 120; Conservative 1
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Best Local Similarity
Matches 107; Conserv
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A,Status: preliminary
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-84,'P',86-1291 <HAU>
A,Residues: 1-84,'P',86-1291 <HAU>
A,Cross-references: UNIPROT:Q93HT3; UNIPARC:UPI000016D75D; EMBL:X53751; NID:g14905; PIDN
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A;Title: The complete nucleotide sequence of the gene coding for botulinum type C-1 toxi A;Reference number: A35396; MUID:91024998; PMID:22224445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP1000003160; EMBL:X62389; NID:g558175; PIDN:CAA44263.1; PI R;Kimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Oguma, K. Appl. Environ. Microbiol. 57, 1168-1172, 1991
A;Title: Cloning of the structural gene for Clostridium botulinum type C-1 toxin and who A;Reference number: A49777; MUID:91282468; PMID:2059039
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C;Accession: S11291; A35396; S22166; A49777
C;Accession: S11291; A35396; S22166; A49777
R;Hauser, D.; Eklund, M.W.; Kurazono, H.; Binz, T.; Niemann, H.; Gill, D.M.; Boquet, Nucleic Acids Res. 18, 4924, 1990
A;Title: Nucleotide sequence of Clostridium botulinum C1 neurotoxin.
A;Reference number: S11291; MUID:90370487; PMID:2204031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGY-NKWPFVTVTNNMMGNMKIYI 1024
     SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      botulinum neurotoxin type C1 precursor - Clostridium botulinum C;Species: Clostridium botulinum
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A,Residues: 1-669.R, 671-1291 <TS1>
A,Cross-references: UNIPARC:UP10000176709
R,Tsuruki, K.; Kimura, K.; Fujii, N.; Vokosawa, N.; Oguma, K. R,Tsuruki, K.; Kimura K. Fujii, N.; Ocember 1991
A,Description: Nucleotide sequence of the gene for one of the
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                                                                                                                                                                                                                           23.9%; Score 546; DB 2; L
31.5%; Pred. No. 8.2e-24;
ive 82; Mismatches 169;
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A; Accession: $22166
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A; Residues: 1-1291 <TS2>
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R; Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.

R; Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.

R; Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.

A; Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolythen the number: $27125; MUID:93063293; PMID:1331807

A; Reference number: $27125; MUID:93063293; PMID:1331807

A; Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin. R; de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.

Bur. J. Biochem. 229, 61-69, 1995

A; Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin. A; Reference number: $69348; MUID:95262688; PMID:7744050

A; Accession: $69348

A; Molecule type: protein

A; Residues: 2-31 < DEF-

A; Cross-references: UNIPRAC:UP100017364F

C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fragual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C; Comment: The precursor is cleaved by endogenous proteinase activity to ganglic C; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is sinternalized c; comment: This potent neurotoxin binds to peripheral neuronal synapses, is sinternalized presentation perion of presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
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A.Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synaph C.Superfamily: tetanus toxin
C.Superfamily: tetanus predicted cTLD-
F.2-457/Product: tentoxylysin light chain (fragment A) #status predicted cTLD-
F.461-1315/Product: tentoxylysin heavy chain (fragment B.C) #status experimental cTTH>
F.461-1315/Promain: channel forming (fragment B) #status predicted cTXB-
F.665-1315/Domain: gangiloside binding (fragment C) #status predicted cTXC-
F.233,237/Binding site: zinc (His) #status predicted
                                                                                                                                                                  the NH-2-terminal
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                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 461-475 MAT>
A; Cross-references: UNDARC: UPD000017364E
A; Cross-references: UNDARC: UPD000017364E
R; Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, J. Imminol. 142, 394-402, 1989
A; Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A; Reference number: US0098; MUID: 89993918; PMID: 2463305
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LKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESSEVIVHKAMD 940
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A,Cross-references: UNIPARC:UPI000017364D
R;Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
Infect: Immun. 57, 3588-3593, 1989
A;Title: Isolation, purification, and characterization of fragment
A;Reference number: A60759; MUID:90035436; PMID:2478476
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Search completed: March 2, 2006, 00:47:40 Job time : 38 secs

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P04958 P18640 Q93ht3 Q93ht3 Q91bt1 Q45967 Q66798 Q45848 Q45888 Q45888 Q66797 Q66797 P7117

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ALIGNMENTS

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121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=bont/f; Synonyms=bonT/F;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elmore M.J. Bodgworth N.J., Whelan S.M., Minton N.P.;
L. Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
R. Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
R. EMBL; ISS48114; CAA57358.1; -; Genomic_DNA.
R. EMBL; LISS46; AAA23210.1; -; Genomic_DNA.
R. FRBS; Q48894; 1E1H.
R. MEROPS; MZT.002; -.
R. GO; GO:0016021; C:integral to membrane; IEA.
R. GO; GO:0006237; F:metallopeptidase activity; IEA.
R. GO; GO:0006237; F:metallopeptidase activity; IEA.
R. GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R. InterPro; IPR001591; Botulinum.
R. InterPro; IPR001595; Peptidase MZ7.
InterPro; PR0016055; Peptidase MZ7.
R. PRINTS; RR00760; BORNOZILYSIN.
R. PRINTS; RR00760; BORNOZILYSIN.
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Hutson R.A., Collins M.D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
BONT/F (Neurotoxin type F);
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100.0%; Pred. No. 6.9e-128;
ive 0; Mismatches 0;
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Q57236; Q45863;
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Q91bs7
                                                                                                                                   2, 2006, 00:32:07; Search time 221 Seconds
                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q7B8V4 CLOBO
BXA2 CLOBO
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Q9K395_CLOBU
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Q8KZM3_CLOBU
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Type F / Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
13-SEP-2005 (Rel. 48, Last ann
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                                                                      1028 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                              SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                           EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                 1148 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                       361 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDLSGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CDC 3281;
MEDLINE=98440323; PubMed=9767710; DOI=10.1007/s002849900384;
Battos-Buelga U., Collins M.D., East A.K.;
"Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B & F neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum.
Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.5%; Score 1887.5; DB 2; Length 1280; 82.4%; Pred. No. 5e-104; ive 32; Mismatches 41; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Santoe-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13631; CAA73972.1; -; Genomic_DNA.
R HSSP; Q5844; IEIH.
R RCOPS; M27.002; -.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008237; F:pathogenesis; IEA.
GO; GO:000837; F:pathogenesis; IEA.
R GO; GO:000839; P:pathogenesis; IEA.
InterPro; IPR011591; Botulinum.
R InterPro; IPR00135; Peptidase M27.
InterPro; IPR005035; Peptidase M27.
InterPro; IPR005035; Peptidase M27.
InterPro; IPR005035; Peptidase M37; I.
R PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PR00142; ZINC_PROTEASE; UNKNOWN I.
R PROSTIE; PS00142; ZINC_PROTEASE; UNKNOWN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr. Microbiol. 37:312-318(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAK-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                Q9ZAJS CLOBO PRELIMINARY;
Q9ZAJS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.4%
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                   1268 FISKEHGWQEN 1278
                                                                                                                                                                                                                                                                                                        431
                                                                                                                                                                                                                                                                                                        FISKEHGWOEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium.
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                                                                                                               241
                                                181
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1148 EGVEVIIRKNAPIDISNTDNFVRKNDLAYINVVDHGVEYRLYADISIIKSEKIIKLIRTS 1207
                                                                                                                                                                                                                                                                                                                                                                                        177
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                            967
                                                                                                                                                                                                                                                                                             298 TGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTS 357
                                                                                                                                                                                                                                                                                                                                                                    358 NSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGC 417
                           GIYSGRLSEVNIAQNNDIIYNSRYQNFSISFWVTIPKHYRPMNRNREYTIINCMGNNNSG
                                                                       121 WKISLNYNK---IIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIY
                                                                                                                                               178 INGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDE
                                                                                                                                                                                                                       PDPSILKDFWGNYLLYNKRYYLLNLLKTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 634-1002.
MEDLINE=4401372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=TYPE F / ATCC 23387;
MEDILINE=33012902; PubMed=1398040; DOI=10.1016/0378-1097(92)90408-G;
East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A.,
Thompson D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    East A.K., Collins M.D.; "Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic Clostridium botulinum type FCurr. Microbiol. 29:69-77(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BONT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1274 AA
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1026

1086

417

357

us-08-981-087b-1.rup

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WKISLNYNK---IIWTLODTAGNNQKLVFNYTOMISISDYINKWIFVTITNNRLGNSRIY 177
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                             298 TGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTS
                                                                                                      INGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDE
                                                                                                                                                                                                       PDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLY
                                                                                                                                                                                                                                                                                                                                                                                                                   NSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence of the gene coding for Clostridium barati type neurotoxin: comparison with other clostridial neurotoxins.", FEMS Microbiol. Lett. 108:175-182(1993).

EMBL; X68262; CAA48329.1; -; Genomic_DNA.

PIR; S33411; S33411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=93252228; PubMed=8486245; DOI=10.1016/0378-1097(93)90581-L;
Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,
Richardson P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium baratii.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1268;
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GO; GO:000827; F:mathalopeptidase activity; IEA.
GO; GO:0008405; P:mathagenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR000359; Peptidase_M27.
PITTERPO: IPR006025; Peptidase_M27.
PEAM; PP01742; Peptidase_M27; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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78.8%; Pred. No. 2e-100;
ive 38; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00760; BONTOXILYSIN
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01,
26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FWSFISKEHGWOE 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q45851 9CLOT PRELIMINARY;
Q45851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q45894; 1E1H.
MEROPS; M27.002; -.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotoxin type F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=bont /f.
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SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418
                                                                                                              178
                                                                                                                                                                                                                    238
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             121
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                                                                                      Detulinal neurotoxins and tetanus toxin.";

1. Biol. Chem. 269:1276-1272(1994).

1. Biol. Chem. 269:1276-12772(1994).

1. FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 58-Gln-|-Lys-59 bond of synaptobrevins-1 and -2.

1. CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

1. CORACTOR: Binds 1 zinc ion per subunit (By similarity).

2. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel community and a community of the state of the community of the chain mediate channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          906
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             Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F., Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.; "Cleavage of members of the synaptobrevin/VAMP family by types D and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR012928; Toxin recet bd.N.
InterPro; IPR012500; Toxin recet bd.N.
InterPro; IPR012500; Toxin trans.
Pfam; PP01742; Peptidase M27; 1.
Pfam; PP07952; Toxin trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botulinum neurotoxin F light chain.
Botulinum neurotoxin F heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interchain (between light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: There are seven antigenically distinct forms botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
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.larity 81.3%; Pred. No. 8.9e-101;
Conservative 33; Mismatches 40; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chains) (Probable).
MW; 5B99756A7438B921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M92906; AAA23263.1; -; Genomic_DNA.
EMBL; S73676; AAC60475.1; -; Genomic_DNA.
EMBL; X70820; CAAS0151.1; -; Genomic_DNA.
EMBL; X70816; CAAS0147.1; -; Genomic_DNA.
PIR; 140813; 140813.
PIR; S48109; S48109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
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Peptidase M27
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InterPro; IPR006025; Pept_M_Zn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1274 AA;
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Matches 352; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS: M27.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    847
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InterPro; IPR012500; Toxin
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                                                                                                                                                                                                                                                      1080 ILKDFWGNYLLYNKKYYLLNLLKPNMSVTKNSDILNINRQRGIYSKTNIFSNARLYTGVE 1139
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                               IYSSRLSEVNITQNNTIIYNSRYQNFSVSFWVRIPKYNNLKNLMNEYTIINCMRNNNSGW 959
                                                                                                                                                                                                                                                                                                                                 1LKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKFNIFSNTRLYTGVE 301
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A Wang X., Macgawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
T. "Genetic analysis of type B botulinum toxin-producing clostridium
T. butyricum strains.";
Appl. Environ. Microbiol. 66:4992-4997 (2000).
E. EMBL, AB037704; BAB03512.1; -; Genomic DNA.
R. EMBL, AB037706; BAB03512.1; -; Genomic DNA.
R. EMBL, AB037706; BAB03513.1; -; Genomic DNA.
R. EMBL, AB037710; BAB03513.1; -; Genomic DNA.
R. EMBL, AB037710; BAB03513.1; -; Genomic DNA.
R. EMBL, AB037711; BAB03512.1; -; Genomic DNA.
R. EMBL, AB037708; BAB03515.1; -; Genomic DNA.
R. EMBL, AB037708; BAB03515.1; -; Genomic DNA.
R. EMBL, AB037708; BAB03515.1; -; Genomic DNA.
R. EMBL, AB037709; BAB03515.1; -; Genomic DNA.
IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
                                                                                                          KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR006025; Pept M. Zn. BS.
InterPro; IPR006395; PeptIdase_M27.
InterPro; IPR012928; Toxin_recpt_bd_N.
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MEDLINE=20509829; PubMed=11055954;
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Q9K395;
Q1-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 15, Li
01-FEB-2005 (TrEMBLrel. 29, Li
Type E botulinum toxin.
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EMBL; AB037708; BAB03516.1;
EMBL; AB037707; BAB03515.1;
HSSP; Q45894; 1E1H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1069 INILKDFWGNYLLYDKGYYLLNVLKPNNFIDRRKDSTLSINNIRS-----TILLANRLYS 1123
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                                                                                                                                                                                                                                                                                                                                                                              61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 889 TIFNSKPSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVNINNEYTIINCMRDNNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 SNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCF
                                                                                                                                                                                                                                                                                                                                                1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                63.7%; Score 1458; DB 2; Length 1251; larity 62.7%; Pred. No. 1.9e-78; Conservative 75; Mismatches 74; Indels 12
                                                                                                                                                   UNKNOWN 1.
2021F4E427070296 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurotoxin type E.
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Pfam; PF01742; Peptidase M27; 1.
Pfam; PF07953; Toxin, R. Bind N; 1.
Pfam; PF07952; Toxin, trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UN SEQUENCE 1251 AA; 143752 MW; 20
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|239 WNFISEEHGWQE 1250
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Q54A79 CLOBO PRELIMINARY;
Q54A79;
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Matches 271; Conserv
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                                61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS
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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis IEA.
GO; GO:0006906; P:pathogenesis IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR000395; Peptidase M27.
InterPro; IPR0000395; Peptidase M27.
InterPro; IRR0000395; Peptidase M27.
InterPro; IRR0000395; Peptidase M27.
InterPro; IRR0000395; Peptidase M37.
IRR00000395; Peptidase M37.
IRR0000395; Peptidase M37.
IRR00000395; Peptidase M37.
IRR0000039
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Last sequence update)
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EMBL; AB039264; BAB12249.1; -; Genomic_DNA.
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MEDLINE=20509829; PubMed=11055954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FAR6_CLOBU PRELIMINARY;
Q9FAR6;
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                                                                                   SYTDDKILLSYFNKFFRRIKSSSVLMMRYKNDKYVDTSGYDSNININGDVYKYPTNKNQF
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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TBUARDHOLO K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa TBUARDHOLO K., Mukamoto M., Kozaki S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB008207; BAC05434.1; -; Genomic_DNA.
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ProDom; PD001963; Botulinum; 1.
PROSTIE; PRO0142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1252 AA; 143510 MW; 41B633BB744D3B41 CRC64;
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GO:0008237; F:metallopeptidase activity; IEA.
GO:0009405; P:pathogenesis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last annotation update)
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63.0%; Pred. No. 1.6e-77;
iive 73; Mismatches 71;
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InterPro; IPR000039; Peptidase_M27.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PF01742; Peptidase_M27; I.
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Best Local Similarity 63.0
Matches 274; Conservative
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Q8KZM3;
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Chem. 265:9153-9158(1990)

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GIKVKIQRVNNSSTN----DNLVRKNDQVYINFVASKTHLLPLYADTATTNKEKTIKI-- 1180
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                                                                   1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNOF
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MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
                                Gaps
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MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
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Q004962, Q004962,
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurocoxin type E precursor (EC 3.4.24.69) (BoNT/E)
(Bonţoxilysin E) [Contains: Botulinum neurotoxin E light chain;
                                17;
                                71; Indels
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            Pred. No. 1.6e-77;
                                Mismatches
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63.0%; F1
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1240 GFFWNFISEEHGWQE 1254
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NUCLEOTIDE SEQUENCE.
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            Similarity
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                            274;
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This Swiss-Prot entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                             Gimenez J.A., Dasgupta B.R.; "Botulinum neurotoxin type B fragmented with endoproteinase Lys-C reveals the site trypsin nicks and homology with tetanus neurotoxin."; Biochimie 72:213-217(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Type E / Hazen 36208;
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., Bast A.K.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Bornenti F., Wilson M.C., Montecucco C.; Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds."; FEBS Lett. 335:99-103(1993).
                                                                                           and
                                                                                                                                                                                                                                MEDLINE=90344918; PubMed=2116911; DOI=10.1016/0300-9084(90)90075-R
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PROTEIN SEQUENCE OF 1-13.
MEDLINE=851979543, Pubmed=9888113;
MEDLINE=81979543, Pubmed=9888113;
MEDLINGE JJ., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neux
                                                                                                                                             Arch. Biochem. Biophys. 238:544-548(1985).
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EMBL; X62683; CAA44558.1; -; Genomic_DNA.
EMBL; X70815; CAA50146.1; -; Genomic_DNA.
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PIR; S21178; S21178.
PDB; 1T3A; X-ray; A/B=1-421.
PDB; 1T3C; X-ray; A/B=1-421.
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STRAIN=BL6340
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Zinc (catalytic) (By similarity).
Interchain (between light and heavy chains) (Probable).
R -> G (in Ref. 2).
C -> S (in Ref. 2).
R -> A (in Ref. 2 and 3).
I -> L (in Ref. 2 and 6).
                                   InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012928; Toxin Lrans.
Pfam; PF07952; Poxin R bind N; 1.
Pfam; PF07952; Toxin Lrans; 1.
Probom; PF001963; Botulinum; 1.
Probom; PB00142; ZINC_PROTRASE; 1.
PROSITE; PS00142; ZINC_PROTRASE; 1.
3D-structure; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
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Botulinum neurotoxin E heavy chain.
By similarity.
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C -> S (in Ref. 2 and 3).

R -> A (in Ref. 2).

I -> L (in Ref. 2 and 6).

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R -> A (in Ref. 2 and 6).

N -> NN (in Ref. 2 and 6).
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Created) Last sequence update) Last annotation update)

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01-JUL-1993 01-JUL-1993 13-SEP-2005

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                                                                                                                                Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
                                       Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E) (Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain; Botulinum neurotoxin E heavy chain].
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EMBL; X53180; CAA37321.1; -; Genomic_DNA.
PIR; JH0256; JH0256.
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InterPro; IPR012500; Toxin_trans
Pfam; PF01742; Peptidase Wa7; 1.
Pfam; PF07953; Toxin_R bind_N; 1.
Pfam; PF07952; Toxin_trans; 1.
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InterPro; IPR000395; PeptIdase_M27
                                                                                                              STRAIN=ATCC 43181, and ATCC 43755;
MEDLINE=92181428; PubMed=1543481;
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PRINTS; PR00760; BONTOXILYSIN
ProDom; PD001963; Botulinum; 1
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SMR; P30995; 1-411
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                                                                         NCBI_TaxID=1492;
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NUCLEOTIDE
   GWKVSLNHNEIIWTLQDNSGINQKLAFNYGNANGISDYINKWIFVTITNDRLGDSKLYIN 1007
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MEDLINE=90235864; PubMed=2185020;
Thompson D.E., Brehm J.K., Oultram J.D., Swinfield T.-J., Shone C.C.,
Atkinson T., Melling J., Minton N.P.;
"The complete amino acid sequence of the Clostridium botulinum type A
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PROSITE; PS00142; ZINC PROTEASE; 1.
Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease;
Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
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1010845; P01561; P18639;
01-JUL-1999 (Rel. 11, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precureor (EC 3.4.24.69) (BoNT/A)
(Bontoxilysin A) (BOTOX) (Contains: Botulinum neurotoxin A light-
                                                                  lytic) (By similarity).
lytic) (By similarity).
(between light and heavy
                                      Botulinum neurotoxin E light chain.
Botulinum neurotoxin E heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
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                                                                                                                                     DB 1; Length 1250;
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                                                                   (catalytic) (By (catalytic) (By
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73; Mismatches 71
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K -> M (in Ref.
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                                                                                                                  1250 AA;
                                                                                                                                              Similarity
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Dasgupta B.R., Foley J., Niece R.; "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
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MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(95)01241-5;
Fujita R., Fujinaga Y., Inoue K.; Nakajima H., Kumon H., Oguma K.;
"Molecular characterization of two forms of nontoxic-nonhemagalutinin components of Clostridium botulinum type A progenitor toxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betley M.J., Somers E., Dasgupta B.R.; "Characterization of botulinum type A neurotoxin gene: delineation of the N-terminal encoding region."; Blochem. Blochem. Blochem. Blochem. Blochem.
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MEDLINE=97016817; PubMed=8863443;

Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteclytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";

Int. J. Syst. Bacteriol. 46:1105-1112(1996).
                                                                                                                                                                                                                                                                                 Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.; "The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins"; "; biol. Chem. 265:9153-9158(1990).
neurotoxin, deduced by nucleotide sequence analysis of the encoding
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MEDLINE=91120847; PubMed=2126206; DOI=10.1016/0300-9084(90)90048-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE-89024662; PubMed-3178218;
Sathymoorthy V., Dasgupta B.R., Foley J., Niece R.L.;
"Botulinum neurotoxin type A: cleavage of the heavy chain into two
halves and their partial sequences.";
Arch. Blochem. Blophys. 266:142-151(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dasgupta B.R., Dekleva M.L.; "Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-84178511, Pubmed-6370252;
Schmidt J.J., Sartymoorthy V., Dasgupta B.R.;
"Partial amino acid sequence of the heavy and light chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 119:900-904(1984)
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[11]
PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
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                                                                                                                                                                                                            STRAIN=Type A / 62A;
MEDLINE=90264400; PubMed=2160960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Type A / Hall;
MEDLINE=89350959; PubMed=2669749;
                                                                              dur. J. Biochem. 189:73-81(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   botulinum neurotoxin type A.";
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1034 LIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNBKEIKDLYDNQSNS 1093
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Botulinum neurotoxin A heavy-chain.
Potential.
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Zinc (catalytic)
X92973; CAA63551.1; -; Genomic_DNA.
D67030; BAA11051.1; -; Genomic_DNA.
M27892; AAA23269.1; -; Genomic_DNA.
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Interpro; IPR006025; Pept M. Zn. BS.
Interpro; IPR0003925; Pept Gase_M27.
Interpro; IPR012928; Toxin recpt bd.
Interpro; IPR012500; Toxin_trans.
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Best Local Similarity
Matches 219; Conserv
                                                                                                                                                                                                                              MEROPS; M27.002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Let Struct. Biol. 5:898-902(1998).

-I. FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gin-l-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain (H).

-!- SUBCELLULAR LOCATION: Secreted.
-!- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
MEDLINES-98455071; PubMed=9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

COFACTOR: Binds 1 zinc ion per subunit.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Niemann H.;
"Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
J. Biol. Chem. 269:1617-1620(1994).
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DATABASE: NAME=Protein Spotlight; NOTE=18sue 19 of February 2002;
WWW="http://www.expasy.org/spotlight/back_issues/sptlt019.shtml".
                                                                                                     72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Botulinum neurotoxins serctypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds.";
FEBS Lett, 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                 MEDLINE-94063091; PubMed-8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  늉
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MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Migori M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
"Site-directed mutagenesis adentifies active-site residues of the light chain of botulinum neurotoxin type a.";
Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
                  PubMed=8397793;
Gimenez J.A., DasGupta B.R.;
Betulinum type A neurotoxin digested with pepsin yields 132, 97,
45, 42, and 18 kD fragments.";
J. Protein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANBOUS: There are seven antigenically distinct forms botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family. DATABASE: NAME=BOTOX product information Web site;
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                                                                                                                                                                                                                                                                                               IDENTIFICATION OF SUBSTRATE.
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(catalytic)

408 IRKNTSSNGCFWSFISKEHGWQE

240

181

12 RESULT

EMBL; X52066; CAA36289.1; -; Genomic\_DNA EMBL; M30196; AAA23262.1; -; Genomic\_DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1095 GILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSL 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           856 YVDNQRLLSTFTEYIKNIINTSILNLKYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQ 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                                                                                       STRAIN-Allergan-Hall A;
MEDLINE-22919384; PubMed-14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zhang L., Lin W.J., Li S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
Clostridium botulinum type A-Hall (Allergan) strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                  Dineen S.S., Bradshaw M., Johnson E.A.; "Neurotoxiding type A strains: "Neurotoxiding type A strains: sequence comparison and evolutionary implications."; Curr. Microbiol. 46:345-352(2003).
                                                                                                                                                                                                                   STRAIN=Hall A-hyper;
MEDLINE=22617869; PubMed=12732962; DOI=10.1007/800284-002-3851-1;
                                                                                                                                 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.4%; Pred. No. 2.0e-50,
tive 78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1296 AA; 149425 MW; DEA8CF2754AE43E6 CRC64;
                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1120.5; DB Pred. No. 2.6e-58;
PRT; 1296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF461540; AAM75961.1; -; Genomic DNA
EMBL, AF488749; AAQ06331.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1271 IERSSRTLGCSWEFIPVDDGWGE 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 IRKNTSSNGCFWSFISKEHGWQE 430
                                                              10-MAY-2005 (TrEMBLrel. 30, BONT/A (Neurotoxin BONT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.04;
                           10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
Q7B8V4_CLOBO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 219; Conservative
                                                                                                 Name=bont/a;
Clostridium botulinum.
                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                   NCBI_TaxID=1491;
                                                                                                                                                    Clostridium.
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PRT; 1295 AA.

STANDARD;

RESULT 13 BXA2\_CLOBO ID BXA2\_CLOBO

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WEDLINE=TYPE A / Kyoto-F:

X STRAIN=TYPE A / Kyoto-F:

X BEDLINE=97016817; PubMed=8863443;

X BETALINE=97016817; PubMed=8863443;

X Components of the botulinum toxin complex in proteolytic clostridium components of the botulinum toxin components of the botulinum toxin components of the botulinum toxin components of the control of cline=10 cline=10 sequences in the botulinum types A, B, and F: evidence of chimeric sequences in the botulinum types A, B, and F: evidence of chimeric sequences in the botulinum types A, B, and F: evidence of chimeric sequences in the botulinum types A, B, and F: evidence of chimeric sequences in the botulinum toxin membrane, is then internalized by receptor-mediated endocytosis.

Y C -1- FUNCTION: Inhibited acetylcholine release and hardence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyses the 19-Gin-1-Arg-198 bond in SNAP-25, thereby blocking neuroexocytosis apparatus, with frequent heart or respiratory failure (By similarity).

C -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

C -1- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity).

-1- SUBURITALINEAR LOCATION: Secreted.

-1- SUBURITALINEAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                STRAIN=TYPE A / Kyoto-F;
MEDLINE=94143603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: There are seven antigenically distinct forms of
                                                                                                                                                                                                                                                                                                                                                                                            Willems A., East A.K., Lawson P.A., Collins M.D.; "Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison with other clostridial neurotoxins.";
                                              28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (BC 3.4.24.69) (BONT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-
                                                                                                                                                                        Name=botA; Synonyms=atx, bna;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             botulinum neurotoxin: Types A, B, Cĭ, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                 chain; Botulinum neurotoxin A heavy-chain].
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BEL; X87974; CAA51234.1; -; Genomic_DNA.
PIR; 140645; 140645.
PDB; 1EIH; X-ray; A/C=9-249; B/D=250-415.
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InterPro; IPR0106025; Pept M Zm BS.
InterPro; IPR010395; Pept Mase M27.
InterPro; IPR0102928; Toxin_recpt_bd_N.
InterPro; IPR012928; Toxin_recpt_bd_N.
InterPro; IPR0129280; Toxin_rens.
Fam; PP0142; Peptidase M27; 1.
Pfam; PP07953; Toxin_R bInd_N; 1.
PRINTS; PR09760; BOXIOXILYSIN.
ProDom; PD001963; Botulinum; 1.
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                       Created)
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                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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Clostridium botulinum
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STRAIN=type F;
                   NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                   e; Toxin; Transmembrane; Zinc.

I 447 Botulinum neurotoxin A light-chain.

448 1295 Botulinum neurotoxin A heavy-chain.

446 646 646 Potential.

522 222 Zinc (catalytic) (By similarity).

226 226 Zinc (catalytic) (By similarity).

226 226 Zinc (catalytic) (By similarity).

227 329 Sinc (catalytic) (By similarity).

228 453 Interchain (between light and heavy chains) (By similarity).

229 453 Sinc (catalytic) (By similarity).

220 220 Zinc (catalytic) (By similarity).

221 222 Zinc (catalytic) (By similarity).

222 223 Sinc (catalytic) (By similarity).

223 224 453 Sinc (catalytic) (By similarity).

224 453 Sinc (catalytic) (By similarity).

225 226 Zinc (catalytic) (By similarity).
PS00142; ZINC_PROTEASE; FALSE_NEG.
.ure; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                         47.7%; Score 1092.5; DB 1; Length 1295; 48.6%; Pred. No. 1.2e-56;
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                                                                                                                                                                                                                                                                                                                                                          48.6%; Pred. No. 1.25-20,
tive 76; Mismatches 133; Indels
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Last annotation update)
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10-MAY-2005 (TrEMBLrel. 30, Last seq
10-MAY-2005 (TrEMBLrel. 30, Last ann
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Q58GH1 CLOBO
ID Q58GH1 CLOBO PRELIMINARY;
AC Q58GH1;
                                                                                                                                                                                                                                                                                                                                                                                       Matches 216; Conservative
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                        3D-structure;
Protease; Toxi
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1095 GILKDFWGNYLQYDKPYYMLNLFDPNKYVDVNNIGIRGYMYLKGPRGSVVTTNIYLNSTL 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN
                                                                                                                                                                                                                                                                                                                                                          2 YTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campbell K.D., Collins M.D., East A.K.; "Genpropers for identification of the botulinal neurotoxin gene and "Gene probes for identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                          19; Gaps
                                                                               1mpacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                    47.7%; Score 1092.5; DB 2; Length 1296;
48.6%; Pred. No. 1.2e-56;
Live 76; Mismatches 133; Indels 19;
                          Tsai R., Tepp W.H.,
rks J.D.;
STRAIN=FRI.HIA2;
Smith T.J., Lou J., Geren I., Forsyth C., Tsai R., Tepp W.:
Smith T.J., Lou J., Geren I., Forsyth C., Tsai R., Tepp W.:
Bradshaw M., Johnson E.A., Smith L.A., Marks J.D.;
"Sequence variation within botulinum neurotoxin serotypes
antibody binding and neutralization.";
submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AY953275; AAX53156.1; -; Genomic_DNA.
Neurotoxin.
                                                                                                                                                                                                       1296 AA; 149410 MW; 6F12E7BF28ED69D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Name=BoNT/F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 IRKNTSSNGCFWSFISKEHGWQEN 431
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MEDLINE=94013372; PubMed=8408542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                    Best Local Similarity 48.6%
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q79AH9_CLOBO PRELIMINARY;
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RA Campbell K.D.;

BL Submitted (JAN.1993) to the EMBL/GenBank/DDBJ databases.

BL Submitted (JAN.1993) to the EMBL/GenBank/DDBJ databases.

BR GO, GO:0009405; P:pathogenesis; IEA.

RA Nourtex

NON TER 366 366

SQ SEQUENCE 366 AA, 43136 MW; 45A132B235D7E640 CRC64;

SQ SEQUENCE 366 AA, 43136 MW; 45A132B235D7E640 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 8.3e-41; Length 366;

Best Local Similarity 100.0%; Pred. No. 8.3e-41; Indels 0; Gaps 0;

Autches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AND TER 366 AB, 43136 MW; ASA132B235D7E640 CRC64;

Qy | 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTWRNQF 273

Qy | 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTWRNQF 273

Qy | 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIDCIRNNNSG 333

Qy | 121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMIS 153

Db 334 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMIS 366
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Search completed: March 2, 2006, 00:46:23 Job time : 224 secs

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2, 2006, 00:46:47; Search time 53 Seconds (without alignments) 672.325 Million cell updates/sec
                                                                                                                                                                                                  US-08-981-087B-1
2288
1 SYTNDKILILYFNKLYKKIK......TSSNGCFWSFISKEHGWQEN 431
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                               572060 seqs, 82675679 residues
                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                       March
                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                 OM protein
                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                              Sequence:
                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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	g	28,	28,	28,	28,	23,	23,	23,	23,	26,	26,	26,	•	219	6	٠	220,	20,	7	~	4	4,	'n	17,	16,	15,	14,	13
	Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
SUMMARIES	QI	JS-08-480-604A-28	IS-08-405-496A-28	US-08-915-136-28	US-09-084-517-28	US-08-480-604A-23	US-08-405-496A-23	US-08-915-136-23	US-09-084-517-23	US-08-480-604A-26	US-08-405-496A-26	JS-08-915-136-26	US-09-084-517-26	JS-10-360-101-219	US-09-288-326A-9	US-09-548-409B-9	US-10-360-101-220	US-09-255-829-20	US-07-618-312A-2	US-08-280-228-2	US-07-618-312A-4	US-08-280-228-4	US-08-668-381A-5	US-08-913-880C-17	US-08-913-880C-16	US-08-913-880C-15	US-08-913-880C-14	US-08-913-880C-13
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de	Query Match Length	49.0	49.0	49.0	49.0	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.7	47.7	44.6	44.6	33.6	29.6	24.3	24.3	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2
	Score	1120.5	1120.5	1120.5	1120.5	1113.5		1113.5	1113.5	1113.5	1113.5	1113.5	1113.5	1092.5	1019.5	1019.5	769	676.5	556	929	553	553	553	553	553	553	553	553
	Result No.	-	8	e	4	S	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	25	26	27

12, Appl 10, Appl 10, Appl 11, Appl 12, Appl 12, Appl 13, Appl 14, Appl 15, Appl 16,
Sequence 1 Sequence 1 Sequence 1 Sequence 8 Sequence 8 Sequence 6 Sequence 6
18-08-913-880C-12 18-08-913-880C-11 18-08-913-880C-10 18-08-913-880C-1 18-09-13-880C-1 18-09-13-880C-1 18-09-146-2 18-09-4417-485D-8 18-09-417-485D-8 18-09-417-485D-8 18-09-417-485D-6 18-09-417-485D-6 18-09-11-136-6 18-09-11-136-6 18-08-915-136-6 18-08-915-136-6 18-09-084-517-6 18-09-084-517-6 18-09-084-517-6 18-09-084-517-6
866 875 1315 452 452 140 140 1210 2710 2710 2710 2710 2710 1381
44444444444444444444444444444444444444
553 553 553 553 553 524 17.5 17.5 189 149 149 149 149 149
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES, 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/480,604A
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MEDIEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/99,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
Sequence 28, Application US/08480604A Patent No. 5736139
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ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
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                                                                                                                                                                                                                                                                                                                                    2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                           19;
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APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                Query Match

49.0%; Score 1120.5; DB 1; Length
Best Local Similarity 49.4%; Pred. No. 9.7e-83;
Matches 219; Conservative 78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
    OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1271 IERSSRTLGCSWEFIPVDDGWGE 1293
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; Sequence 28, Application US/08405496A
; Patent No. 5919665
REFERENCE/DOCKET NUMBER: OPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                    TYPE: amino acid
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182 LIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.0%; Score 1120.5; DB 1;
49.4%; Pred. No. 9.7e-83;
:ive 78; Mismatches 127;
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 48
FILING DATE: 25-0CT-1994
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,321
FILING DATE: 31-0CT-1889
FILING DATE: 31-0CT-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERENCE/DOCKET NUMBER: 0PHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IERSSRTLGCSWEFIPVDDGWGE 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 49.4%;
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-405-496A-28
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357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQORGVYQKPNIFSNTRL 296
                                                                                                                            297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND EXPLINENT ON OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMENT STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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PRICATION NUMBER: US 08/329,154
PRICATION DATE: 25-0CT-1994
PRICATION DATA:
APPLICATION NUMBER: US 08/161,907
PRICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
PRICATION NUMBER: US 07/985,321
PRICATION NUMBER: US 07/995,321
PRICATION NUMBER: US 07/995,321
PRICATION NUMBER: US 07/99791
PRILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    408 IRKNISSNGCFWSFISKEHGWQE 430
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APPLICATION NUMBER: US/09/084,517
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-084-517-28
; Sequence 28, Application US/09084517
; Patent No. 6613329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
RATOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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49.0%; Score 1120.5; DB 2; Length 1296;
Best Local Similarity 49.4%; Pred. No. 9.7e-83;
Matches 219; Conservative 78; Mismatches 127; Indels 19;
                STAFFORD, DOUGLAS C. FENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND FENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
TURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                             TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TITLE OF INVENTION: PREVENTION OF C. DIFFICI NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSES: MEDLER: MEDLER: MEDLER: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELLICATION DATA:
APPLICATION NUMBER: US 08/405,496
PILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989
ATTICNEY AGENT INFORMATION:
NAME: INGOLAR DATAE
NAME: NAME: OF DEC-1992
NAME: NAME: OF DEC-1993
NAME: NAME: OF DEC-1994
NAME: NAME: OF DEC-1995
NAME: NAME: OF DEC-1995
NAME: NAME: NAME: OF DEC-1995
NAME: NAME: OF
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                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
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TELEPHONE: (415) 705-8410
TELEPRAK: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
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REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPP
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amino acid
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                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
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US-08-480-604A-23
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                                                                                                                                                                                                                                           LENLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW 974
                                                                                                                                                                                                                       122 KISLNYNKIIWTLODTAGNNOKLVFNYTOMISISDYINKWIFVTITNNRLGNSRIYINGN 181
                                                                                                                                                                                                                                                                                               LIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
                                                                                                                                              62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
                                                                          2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08480604A
Patent No. 5736139
GENERAL INFORMATION:
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDIEN & CARROLL, ILP
                                      19;
Length 1296;
49.0%; Score 1120.5; DB 2; Length 49.4%; Pred. No. 9.7e-83; Live 78; Mismatches 127; Indels
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APPLICATION NUMBER: US/08/480,604A FILING DATE: O'-JUN-1995 CLASSIFICATION: 4.24
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STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    Matches 219; Conservative
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Query Match
Best Local Similarity
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US-08-480-604A-23
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123 GEIIWTLODTOBIKORVVFKYSOMINISDYINRWIFVTITNNRLNNSKIYINGRLIDOKP 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 WGNYLLYNKRYYLLNLLRIDKSITQNS----NFLNINQORGVYQKPNIFSNTRLYTGVEV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 LGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 ISNLGNIHASNNIMFKLDGCRDTHRYIMIKYFNLFDKELNEKEIKDLYDNQSNSGILKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LISTFIEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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; Patent No. 5919665
; GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: NACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.7%; Score 1113.5; DB 1; Best Local Similarity 49.9%; Pred. No. 8.5e-83; Matches 218; Conservative 75; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                 NAME: INGOLIA, DIANE E.
REGISTRATION VIMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELEPANTUNICATION INFORMATION:
TELEPANE: (415) 705-8410
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                   APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
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359 LSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSR 418
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                                                                                                                                                                                                                                                                               APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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48.7%; Score 1113.5; DB 2;
Best Local Similarity 49.9%; Pred. No. 8.5e-83;
Matches 218; Conservative 75; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONIFOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING APPLICATION NUMBER: US 08/405,496
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-007-1994
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
FILING DATE: 03-DEC-1993
FILING DATE: 04-DEC-1992
FILING DATE: 04-DEC-1992
FILING DATE: 31-007-1993
ATORNEY MEGNET INFORMATION:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-007-1993
ATORNEY AGENT INFORMATION:
NAME: INFORMATION:
NAME: 1000LIA, DIAME E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  Sequence 23, Application US/08915136 Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/480,604
                                               414 SNGCFWSFISKEHGWQE 430
                                                                                                 419 TLGCSWEFIPVDDGWGE 435
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 438 amino acids
amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 IIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 48.7%; Score 1113.5; DB 1; Length Best Local Similarity 49.9%; Pred. No. 8.5e-83; Matches 218; Conservative 75; Mismatches 125; Indels
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 16-MAR.1995
CLASSIFICATION: 424
                                                    : 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
PRIOR DATE: 25-0CT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
PRIOR DATE: 02-DC-1993
PRIOR DATE: 02-DC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION DATE: 04-DC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
APPLICATION NUMBER: US 07/429,791
REGISTRATION NUMBER: US 07/429,791
REGISTRATION NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                     CARROLL, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 amino acids
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MOLECULE TYPE: protein
            CORRESPONDENCE ADDRESS:
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                                                                                CITY: SAN
STATE: CA
COUNTRY:
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243 WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKF 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 ISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNOSNSGILKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 WGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRLYTGVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 LGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PAPPLYE, NISHA V.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                    Length 438;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                            75; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                 48.7%; Score 1113.5; 49.9%; Pred. No. 8.5e
                                                                                 REFERENCE/DOCKET NUMBER: OPHD-01610 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEPHONE: (415) 397-8338 INFORMATION FOR SEQ ID NO: 23; SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 26, Application US/08480604A; Patent No. 5736139; GENERAL INFORMATION:
                                                                    32,837
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FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                     438 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Best Local Siminary,
Matches 218; Conservative
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
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                                                                                                                                                                                                                     LENGTH:
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                                                                                      SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
                                                                                                                                                                       NKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKS 187
                                                                                                                                                                                                                                                                                                                                                 WGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRLYTGVEV 302
                           LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
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; Sequence 23, Application US/09084517
; Patent No. 6613329
; GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TRE
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DIS
NUMBER OF SEQUENCES: 30
CORRESCED: ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/084,517 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
RRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 02-DEC-1993
FRICR APPLICATION NUMBER: US 07/995,321
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/995,321
FILING APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 SNGCFWSFISKEHGWQE 430
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128 NKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKS 187
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                                                                                                                                               Sequence 26, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/405,496A FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                            SSEE: MEDLEN & CARROLL, LLP
T: 220 MONTCOMERY STREET, SUITE 2200
SAN FRANCISCO
: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154

FILING DATE: 25-CCT-1994

PRIOR APPLICATION NUMBER: US 08/161,907

PILING DATE: 02-DEC-1993

PRIOR APPLICATION NUMBER: US 07/985,321

RILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321

FILING DATE: 31-CCT-1992

RILING DATE: 31-CCT-1989

ATTORNEY/AGENT INFORMATION:
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REGISTRATION UNDRER: 40,027
REFERENCE, DOCKET NUMBER: OPHD
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 797-838
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: Floppy disk
IBM PC compatible
                  414 SNGCFWSFISKEHGWOE 430
                                          : || | | : || |
443 TLGCSWEFIPVDDGWGE 459
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Best Local Similarity 49.9
Matches 218; Conservative
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                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3(
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & (
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/480,604A
                                                                                                                                                                                                                                                                                                                   PRICATION NUMBER: US 08/329,154
PRIOR DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          PRIOR APPLICATION 1213.

APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                         UMBER: US/08/480,604A
07-JUN-1995
                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: TVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 462 amino acids
amino acid
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                                                                                                                                          FILING DATE: 0
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COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
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; Sequence 26, Application US/09084517
; Patent No. 6613329
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 SNGCFWSFISKEHGWQE 430
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                                                                                                                                            ; MOLECULE TYPE: protein US-08-915-136-26
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
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Best Local Similarity
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                                  207 ISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDF 266
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                                                                                                                                                                  IIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS 362
                                                                                                                                                                                         WGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRLYTGVEV 302
                                                                                                                                                                                                                                               LGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS 413
          ISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08915136
Patent No. 6290960
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH N.
APPLICANT: FIRCA, JOSEPH N.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
FILING DATE: 16-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1997
FILING DATE: 04-DEC-1997
FILING DATE: 04-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                     : || | || : || | TLGCSWEFIPVDDGWGE 459
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STATE: CALIFORNIA
COUNTRY: UNITED STAT
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                                                                                                                                                                                                                                                                                 88 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYIIINCM-ENNSGWKVSLNY
                                                                                                                     8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP
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48.7%; Score 1113.5; DB 2; Length 462;
49.9%; Pred. No. 9.2e-83;
tive 75; Mismatches 125; Indels 19;
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APPLICANT: KINK, JOHN A.
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: ISM PC comparatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
FILING DATE:
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APPLICANT: Leenhouts, Cornells J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
FILE REPERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.1
LENGIN 0.219
LENGIN 0.219
TYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
47.7%; Score 1092.5; DB 2;
Best Local Similarity 48.6%; Pred. No. 1.1e-80;
Matches 216; Conservative 76; Mismatches 133;
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APPLICANT: Steward, Lance E.
APPLICANT: Sachs, George
APPLICANT: Sachs, George
TITLE OF INVENTION: Methods and Compositions for tritle OF INVENTION: Methods and Compositions for tritle OF INVENTION: Treatment of Pancreatitis
FILE BEFERENCE: 17282
CURRENT APPLICATION NUMBER: US/09/288,326A
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ. ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 IRKNTSSNGCFWSFISKEHGWQEN 431
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                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-360-101-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-288-326A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKF 326
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49.9%; Pred. No. 9.2e
:ive 75; Mismatches
                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-0EC-1993
PRICA APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-0EC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01610
                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
FILING DATE: 25-0CT-1994
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TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 218; Conservative
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GILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSL 240
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                                                                                                                                                                                                        KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN 181
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                                                                                                                                                        IFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW
                                                                                                                                  62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
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                                                             Length 382;
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; Pred. No. 3.4e-75;
65; Mismatches 102; Indels
                                                                                              102, Indels
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APPLICANT: Sachs, K. Roger
APPLICANT: Sachs, George
APPLICANT: Sachs, George
TITLE OF INVENTION: Treament of Pancreatitis
FILE REPERENCE: 17282CIF(AP)
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 09/288,326
PRIOR APPLICATION NUMBER: US 09/288,326
PRIOR APPLICATION NUMBER: US 09/288,326
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FREESE for Windows Version 3.0
                                                         Query Match
44.6%; Score 1019.5; DB 2;
Best Local Similarity 51.4%; Pred. No. 3.4e-75;
Matches 197; Conservative 65; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09548409B; Patent No. 6843998; GENERAL INFORMATION:
; ORGANISM: Clostridium Botilinum US-09-288-326A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Clostridium botulinum
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Best Local Similarity 51.4%;
Matches 197; Conservative 6
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Best Local Similarity
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US-09-548-409B-9
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121 LIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNS 180
                                            241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
                                                                                                                                      297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                 241 YRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEI 297
                                                                                                                                                                                                                                                              298 PDVGN-LSQVVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQ 356
                                                                                                                                                                                                                                 357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
                                                                         181 GILKDFWGDYLQYDKPYYMLNLYDPNKYYDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSL
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MOLECULE TYPE: peptide US-08-981-087A-1
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1 SYTNDKILILYPNKLYKKIK.....TSSNGCFWSFISKEHGWQEN
                                                                      March 2, 2006, 01:11:03 ; Search time 171.5 Seconds
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.: /cgnz 6/ptodata/1/pubpa/USO/_PUBCOMB.ppp:*
.: /cgnz 6/ptodata/1/pubpaa/USO8
.: /cgnz 6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp:*
.: /cgnz 6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
.: /cgnz 6/ptodata/1/pubpaa/USIOA_PUBCOMB.ppp:*
.: /cgnz 6/ptodata/1/pubpaa/USIOB_PUBCOMB.ppp:*
.: /cgnz 6/ptodata/1/pubpaa/USIOB_PUBCOMB.ppp:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-452-024-152
US-10-205-516-12
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US-10-478-516-7
US-10-130-973A-7
US-10-130-973A-4
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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seq length: 200000000
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        28
        1833
        80.1
        1274
        5
        US-10-728-696-71
        Sequence 71, Appl 20

        29
        1833
        80.1
        1274
        6
        US-11-001-241-71
        Sequence 71, Appl 30

        31
        1800
        78.7
        448
        4
        US-10-354-774-73
        Sequence 71, Appl 34

        32
        1800
        78.7
        448
        4
        US-10-221-33
        Sequence 73, Appl 34

        34
        1800
        78.7
        448
        4
        US-10-729-122-73
        Sequence 73, Appl 36

        35
        1800
        78.7
        448
        5
        US-10-729-122-73
        Sequence 73, Appl 36

        36
        1800
        78.7
        448
        5
        US-10-729-123
        Sequence 73, Appl 36

        37
        1800
        78.7
        448
        5
        US-10-729-527-73
        Sequence 73, Appl 36

        38
        1800
        78.7
        448
        5
        US-10-729-527-73
        Sequence 73, Appl 36

        39
        1458
        6
        US-11-721-728-989-73
        Sequence 73, Appl 36

        41
        1457.5
        63.7
        448
        6
        US-11-012-1
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### ALIGNMENTS

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US-08-91-087A-1
Sequence 1, Application US/08981087A
PUblication No. US20020081304A1
GENERAL INFORMATION:
APPLICANT: Blucre, Michael J.
APPLICANT: Blucre, Michael J.
APPLICANT: Marchine, Margaret L.
APPLICANT: Passechnik, Vladimir A.
APPLICANT: Passechnik, Vladimir A.
APPLICANT: Passechnik, Vladimir A.
APPLICANT: Piball, Fiball, Fib
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           Length 431;
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US-OUS-JULEAR-LE.

SEQUENCE 16, Application US/09910186A
PUBLICATION NO. US20030009025A1
APPLICAMT: U.S. ATMY Medical Research & Material Command
APPLICAMT: U.S. ATMY Medical Research & Material Command
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
FILE REFERENCE: A3326-A
CURRENT FILING DATE: 2001-07-20
PRIOR PELING DATE: 2001-07-20
PRIOR PELING DATE: 2000-05-12
PRIOR FILING DATE: 2000-07-06
PRIOR PELING DATE: 1999-05-12
PRIOR PELING DATE: 1999-05-12
PRIOR PELING DATE: 1999-05-12
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PRIOR PELING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,869
PRIOR PELING DATE: 1999-05-12
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PRIOR APPLICATION NUMBER: 60/133,873
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PRIOR PELING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,873
PRIOR PELING DATE: 1999-05-12
                                                             Indels
     100.0%; Score 2288; DB 2;
100.0%; Pred. No. 1.2e-154;
ive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
Query Match
Best Local Similarity 100.
Matches 431; Conservative
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Sequence 34, Application US/09910186A

Publication No. US20030009025A1

GENERAL INFORMATION:

APPLICANT: U.S. Army Medical Research & Material Command

TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM

TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM

TITLE OF INVENTION: NEUROTOXIN

FILE REFERENCE: A33626-A 067252.0107

CURRENT PILING DATE: 2001-07-20

PRIOR PILING DATE: 2001-07-20

PRIOR PILING DATE: 1990-05-12

PRIOR PILING DATE: 1999-05-12

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                                                                                       100.0%; Score 2288; DB 3; 100.0%; Pred. No. 1.2e-154;
                                                                                                                                                         0; Mismatches
OTHER INFORMATION: Synthetic Construct
                                                                                                                      Best Local Similarity 100.(
Matches 431; Conservative
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US-09-910-186A-16
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                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                              302 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKLIKLIRTSNSN 361
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                          GIYSSKRSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                        NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                               SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                 242 SILKDFWGNYLLYNKRYYLLNLKRTDKSITQNSNFLNINQORGVYQKPNIFSNTRLYTGV
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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100.0%; Pred. No. 1.9e-154;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Staton, John
TITLE OF INVENTION: Constructs for Delivery of
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: DCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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Matches 431; Conservative
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APPLICANT: Maksymowych, Andrew
TILLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-9601
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                                                                                                            100.0%; Score 2288; DB 3; Length 432; 100.0%; Pred. No. 1.2e-154; ive 0; Mismatches 0; Indels 0
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CURRENT FILING DATE: 2003-06-02
ENTING APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 188
                                                      ; OTHER INFORMATION: Synthetic Construct US-09-910-186A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 178, Application US/10452024
Publication No. US20040013687A1
GENERAL INFORMATION:
APPLICANT: Simpson, Lance
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Best Local Similarity 100.0%;
Matches 431; Conservative 0
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       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 431; Conservative
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; OTHER INFORMATION: thrombin linker, diphtheria toxin translocation domain, BoNT/F-HQ
US-10-478-516-6
                                                                                                                                                                                                                            Sequence 6, Application US/10478516;
Sequence 6, Application WS/10478516;
Publication No. US20040208889A1
GENREAL INFORMATION:
APPLICANT: Sutton, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.100000
CURRENT APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LIBRICH: 657
  420
                            575 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 634
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US-10-479-516-5

Jecupate 5, Application US/10478516

Publication No. US200402088931

GENERAL INFORMATION:

APPLICANT:

APPLICANT: Suton, John M.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

FILE REFERENCE: 1581.1000000

CURRENT APPLICATION NUMBER: US/10/478,516

CURRENT FILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: GB 0112687.9

PRIOR PILING DATE: 2001-05-21

PRIOR PLING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Version 3.1

SEQ ID NOS: 32
                                                            SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
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395 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
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                                                                                         SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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APPLICANT: Shone, Clifford
APPLICANT: Shone, Clifford
APPLICANT: Shone, Closerouch John
APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Sutton, Migel
APPLICANT: Sutton, Migel
FILE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: PCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 2000-04-07
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100.0%; Pred. No. 2e-154;
tive 0; Mismatches 0
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 00858.7
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VETSION 3.0
      PCT/GB00/04644
                                                                                                                                                                                                                                                                                             OTHER INFORMATION: synthetic construct
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 100.C
Matches 431; Conservative
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US-10-130-973A-4
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; OTHER INFORMATION: factor Xa linker, diphtheria toxin translocation domain, BONT/F-H
US-10-478-516-7
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Publication No. US20030147895A1
GENERAL INFORMATION
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GENERAL INFORMATION
APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
                                                                                                                                         Secreted Bacterial Effector Proteins
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100.0%; Pred. No. 1.9e-154;
trive 0; Mismatches 0;
                         Sequence 7, Application US/10478516
Publication No. US20040208889A1
GERREAL INFORMATION:
APPLICANT: Sutton, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of SecTILE REFERENCE: 1581.1000000
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT APPLICATION NUMBER: US/10/478,516
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR PILING DATE: 2002-05-21
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENT VORTSION 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 431; Conservative
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yequence 26, Application US/10478516

publication No. US2004020889A1

GENERAL INFORMATION:

APPLICANT: Sthone, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

TITLE OF INVENTION NUMBER: US/10/478,516

CURRENT APPLICATION NUMBER: PCT/GB02/02384

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 32

SOUTWARE: Patentin version 3.1

SEQ ID NO 26

TYPER: PATENTIAL OF SEQ ID NOS: 32

SEQ ID NO 26

TYPER: PATENTIAL OF SEQ ID NOS: 32

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SEQ ID NO 26

TYPER: PRIOR TILING DATE: 2002-05-24

TYPER: PATENTIAL OF SEQ ID NOS: 32

SEQ ID NO 26

TYPER: PRIOR TILING DATE: 2003-05-24

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; Pred. No. 2.7e-154;
0; Mismatches 0;
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Query Match
Best Local Similarity 100.0%;
Matches 431; Conservative 0
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APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
SEQ ID NO 6
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                                                                                                                                                                                                           100.0%; Score 2288; DB 4; 100.0%; Pred. No. 2.6e-154;
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                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 431; Conservative
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
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                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR PILING DATE: 2000-12-04
PRIOR PILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-13-07
PRIOR FILING DATE: 1999-13-07
PRIOR FILING DATE: 1999-13-07
NUMBER: OF SEQ ID NOS: 18
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10130973A Publication No. US20030147895A1 GENERAL INFORMATION:
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APPLICANT: Shone, Clifford
APPLICANT: Shone, Clifford
APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: CONSTRUCTS for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT PILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: ECT/GB00/04644
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 2000-04-07
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WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
                                                                                                             NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
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Pred. No. 3.3e-154;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/10130973A Publication No. US20030147895A1 GENERAL INFORMATION:
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100.0%; Pri
tive 0; 1
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SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 1032
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Matches 431; Conservative
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OTHER INFORMATION: Protein sequence for SigD with the first 29 codons removed, throm OTHER INFORMATION: linker,
OTHER INFORMATION: diphtheria toxin translocation domain, with BONT/F-HC
US-10-478-516-23
                                                                                                                                                                                                                        Sequence 23, Application US/10478516

Publication No. US2004020889A1

GENERAL INFORMATION:

APPLICANT: Sutton, John M.

APPLICANT: Shone, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

FILE REFERENCE: 1581.1000000

CURRENT APPLICATION NUMBER: US/10/478,516

CURRENT PILING DATE: 2003-11-24

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Version 3.1
1022 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 1081
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ORGANISM: Artificial sequence
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Search completed: March 2, 2006, 01:17:47

Job time : 173.5 secs

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March 2, 2006, 01:12:18 ; Search time 17.5 Seconds
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491.279 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Sequence 5, Appli	Sequence 8, Appli	Sequence 28, Appl	26,	Sequence 18, Appl	Sequence 3, Appli	Sequence 6, Appli	Sequence 20, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 30, Appl	20,	Sequence 24, Appl	Sequence 141, App	Sequence 22, Appl	339,	Sequence 171, App	Sequence 41, Appl	Sequence 91, Appl	Sequence 42, Appl	Sequence 10263, A		Sequence 90, Appl	6053	Sequence 216, App
SUMMAKIES	ΩI	US/11/062	US/11/062	US-10-909-769-28	US-10-909-769-26	US-10-909-769-18	US/11/062	US/11/062	US-10-909-769-20	US/11/062	US/11/062	US-10-909-769-30	US-11-077-550-20	US-10-909-769-24	US-11-077-550-141	US-10-909-769-22	US-11-052-554A-339	US-11-052-554A-171	US-11-051-453-41	US-11-052-554A-91	US-11-051-453-42	US-11-087-099-10263	US-11-087-099-1756	US-11-052-554A-90	US-11-087-099-6053	US-10-485-517-216
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d	Query Match	100.0	100.0	80.1	63.7	49.0	49.0	49.0	34.1	33.6	33.6	32.2	29.6	25.4	24.2	23.9	7.0	6.5	6.4	5.9	5.6	S	5.5	5.5	5.5	5.2
	Score	2288	2288	1833	1457.5	1120.5	1120.5	<b>3</b> ,120.5	781	769	169	736.5	676.5	580.5	553	546	160	149.5	147	135	129	126	125.5	125.5	125	120
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Sequence 351, App Sequence 200, App Sequence 1, Appli Sequence 482. App		Sequence 126, App Sequence 130, App Sequence 124, App Sequence 132, App		Sequence 5548, Ap Sequence 164, App Sequence 604, App Sequence 11042, A
US-10-485-517-351 US-10-485-517-200 US-11-052-554A-1 US-110-791-676-482	US-110-73-26-48-83 US-11-052-554A-83 US-11-052-554A-92 US-11-131-479-22 US-11-077-550-128	US-11-077-550-126 US-11-077-550-130 US-11-077-550-124 US-11-077-550-132	US-11-077-550-116 US-11-077-550-120 US-11-077-550-122 US-11-077-550-118	US-11-087-099-5548 US-10-873-528-164 US-10-793-626-604 US-11-087-099-11042
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# ALIGNMENTS

RESULT 1 US/11/062 SEQUENC SEQUENC PUBLICA APPLIC APPLIC APPLIC TITLE FILE R CURREN CURREN CURREN CURREN FRIOR PRIOR PRI	SGULT 1 //11/062 //1/
, o , o , us/11,	) TENTAL INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker, US/11/062,471A-5
Que Bes Mat	Query Match Best Local Similarity 100.0%; Score 2288; DB 7; Length 1059; Best Local Similarity 100.0%; Pred. No. 3.4e-160; Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
& a	1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIXSTNRNQF 60 
상 됨	61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 
중 음	121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180 
රු සි	181 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 240 

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Sequence 28, Application US/10909769

Publication No. US20060024331A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Acki, Rei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: 3104-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Version 3.3
SOFTWARE: Patentin Version 3.3
SEQ ID NO 28
LENGTH: 938
EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 1013
                                                                1014 NSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGPHSNNLVASSWYYNNIRKNTSSNGCFWS 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 PDPSILKDFWGNYLLYNKRYYLLINLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710 EGVEVIIRKNGPIDISNTDNFVRKNDLAYINVVDRGVEYRLYAD---TKSEK-EKIIRTS 765
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                                    NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-28
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                                                                                                                                                                          989 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLIGFHSNNLVASSWYNNNTRKNTSSNGCFWS 1048
                                                                                 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                      NSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutage to Neuronal Cells
FILE REFERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 11
SEQ ID NOS A
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                                SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
           SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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' Publication No. US20050255093A1
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Best Local Similarity
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APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel:
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
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49.0%; Score 1120.5; DB 6;
Best Local Similarity 49.4%; Pred. No. 1.1e-74;
Matches 219; Conservative 78; Mismatches 127;
                                                                                                                                                    OTHER INFORMATION: Amino acid sequence of HC
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2004-08-02
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                    NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 18
LENGTH: 849
                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver.
  CURRENT FILING DATE:
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    APPLICANT: Steward, Lance E.

APPLICANT: Lin, Wei-Jen

APPLICANT: Aoki, Kei Roger

APPLICANT: Sachs, George

TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist

FILE REFERENCE: ALLE0010-100 (RO12003-146)

CURRENT APPLICATION NUMBER: US/10/909,769

CURRENT APPLICATION NUMBER: US/10/909,769

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.3

SEQ ID NO 26

LENGHT: 829

TYPE. non.
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APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
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                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Amino acid sequence of HC
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CURRENT APPLICATION NUMBER: US/10/909,769
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Publication No. US20060024331A1
GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
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Lin, Wei-Jen
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Sachs, George
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris
FILE REFERENCE: ALLE0010-100 (ROI2003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                           118 NSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIY 177
                                                                                                                                                                                                                                                YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                            357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
                            GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNN
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                                                                                                 122 KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN
                                                                                                                                                                     2 YTNDKILILYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNOFG
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                                                                                                                                                                                                                                                                                                                     62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANNEYTIIDCIRNNNSGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 IRKNTSSNGCFWSFISKEHGWQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 174; Conservat
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; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker.
US/11/062,471A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal
FILE REFERENCE: 1581.0800001
CURRENT FILING DATE: 1090-11/06
PRIOR PAPLICATION NUMBER: 09/831,050
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                 687 LFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW 745
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                                                                                                                                                                                                                IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
                                                                                                                                          2 YTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
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49.0%; Score 1120.5; DB 7; Length 1092;
Best Local Similarity 49.4%; Pred. No. 1.4e-74;
Matches 219; Conservative 78; Mismatches 127; Indels 19;
                                                                   Length 1067;
                                                                                                         19;
                                                                 ; Score 1120.5; DB 7; Length
; Pred. No. 1.4e-74;
78; Mismatches 127; Indels
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                                                                       49.0%;
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                                                                     Query Match
Best Local Similarity
Matches 219; Conserv
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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human N
US/11/062,471A-7
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                                                                                                        341 DISIAKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNPQNN--NGGNIGLLGFH- 394
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-----LYIGEKFIIRRKSNSQSIN-DDIVRKEDYIYLDFFNLNQEWRVYT 961
858 SYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRD 917
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                                  281 ORGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYA
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
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                                                                                                                                                                                   -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWOE 430
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llarity 36.0%; Pred. No. 8.5e-49;
Conservative 88; Mismatches 152;
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CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: 09/831,050
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1998-11-05
NUMBER: OF SEQ ID NOS: 11
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHONE, Clifford Charles
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169; Conserva
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Best Local S
Matches 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                             JULIANT SUCREMENTATIONS:
APPLICANT: SUNDE, CLIFFORD CHARLES
APPLICANT: SUNDE, CLIFFORD CHARLES
APPLICANT: SUNDE, CLIPS
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE REFERENCE: 1581.0800001
CURRENT FILING NUMBER: US/11/062,471A
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: CT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.1
                                                280 QQRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLY 339
                           INGNLIDEKSISNLGDIHVSDNILPKIVGCND-TRYVGIRYPKVPDTELGKTEIETLYSD 236
                                                                                                EPDPSILKDFWGNYLLYNKRYYLLNL-----LRTDKSI-----TQNSNFLNIN 279
                                                                                                                                                                                                                                                 340 ADISIAKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH 394
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33.6%; Score 769; DB 7; Length 1070;
Best Local Similarity 36.0%; Pred. No. 8.2e-49;
Matches 169; Conservative 88; Mismatches 152; Indels 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
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RESULT 13
US-10-909-769-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REPERENCE: ALLEGOID-100 (RO12003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
987 YKYFKKEEBKLFLAPISDSDBFYNTIQIKEYDEQPTYSCQLLFKKDEBSTDEIGLIGIHR 1046
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                                                                                                                                                      1047 FYESGIVFEEYKDYFCISKWYLKEVRRPYNLKLGCNWQFIPKDEGWTE 1095
                                                                                                         ---SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQE 430
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                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
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US-11-077-550-20
Sequence 20, Application US/11077550
Publication No. US20050244435Al
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SOFTWARE: Patentin version 3.3
SEQ ID NO 30
LENGTH: 855
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Best Local Similarity 35.7*
Matches 164; Conservative
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Aoki, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterists
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APPLICANT: Shout, Conrad Padraig
APPLICANT: Guinn, Conrad Padraig
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Statton, J. Mark
APPLICANT: Statton, J. Mark
APPLICANT: Rayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REPRENEUG: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2002-09-12
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: POT/GB97/02273
PRIOR APPLICATION NUMBER: POT/GB97/02273
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR APPLICATION NUMBER: 1996-12-17
PRIOR PLING DATE: 1996-12-17
PRIOR PLING DATE: 1996-12-17
PRIOR PLING DATE: 1996-12-17
PRIOR PLING DATE: 1996-12-17
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR PLING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR PLING DATE: 1996-03
NUMBER OF SEQ ID NOS: 179
SEQ ID NO 20
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Best Local Similarity 40.6%; Pred. No. 5.5e-42;
Matches 141; Conservative 66; Mismatches 99;
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Publication No. US20060024331A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 PSILKDFWGNYLLYNKRYYLLMLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTG 299
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                                                                                                                                                                                                                                                                                                                                                               GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                     Query Match 25.4%; Score 580.5; DB 6; Length 834; Best Local Similarity 29.4%; Pred. No. 4e-35; Matches 140; Conservative 88; Mismatches 156; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                      ; OTHER INFORMATION: Amino acid seqence of HC US-10-909-769-24
CURRENT FILING DATE: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 24
LENGTH: 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/255,829
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: PCT/GB97/02273
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 141, Application US/11077550
Publication No. US20050244435A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shome, Clifford Charles APPLICANT: Quinn, Conrad Padraig APPLICANT: Foster, Keith Alan APPLICANT: Chaddock, John APPLICANT: Marks, Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 -YNNIRKNTS------
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Stancombe, Patrick
                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jance E.
APPLICANT: Lin, Wei-Jance E.
APPLICANT: Lin, Wei-Jance E.
APPLICANT: Sachs, George
FILE REFERENCE: ALLEGOLO-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT APPLICATION NUMBER: US/10/909,769
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1218 FNNLDRIL---RVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQ 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 IIWTLQDTAGNNQKLVFNYTQMISISD----YI-NKWIFVTITNNRLGNSRIYINGNLID 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 EKSISNLGDIHVSDNILFKIVGC-NDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSIL
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                                                                                                                                                                                                                                                                                                                            Length 1315;
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches 151;
                                                                                                                                                                                                                                                                                                                              24.2%; Score 553; DB 7; 30.2%; Pred. No. 7.2e-33;
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                   PRIOR FILING DATE: 1996-12-27
PRIOR APPLICATION NUMBER: GB962596.5
PRIOR FILING DATE: 1996-12-13
PRIOR PELING DATE: 1996-12-13
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PATCHTIN VERSION 3.1
SEQ ID NO 141
APPLICATION NUMBER: 08/782,893
                                                                                                                                                                                                                                                                                                                                                                             92;
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                                                                                                                                                                                                                                                          ORGANISM: Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 30.29
Matches 139; Conservative
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US-10-909-769-22

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230 IETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPN 289
                                                                                                                                                                                                                                 290 IFSNTRLYTGVEVIIRK-NGSTDISNTDNFVRKNDLAYINVVDRDVEYRL-----YAD 341
                                                                                                                                                                                                                                                                             743 NHSTEDIYAIGLREQTKDI------NDNIIFQIQPMNNTYYYASQIFKSNFNGENISGI 795
                                                                                                                                                                           179 NGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYV-----GIRYFKVFDTELGKTE 229
                                                                                                                                                                                                                                                                                                           342 -----ISIAKPEKIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNN-NGGNI-GL 390
                                             1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60
                        Gaps
                        99
  23.9%; Score 546; DB 6; Length 842; 31.5%; Pred. No. 1.4e-32; Live 82; Mismatches 169; Indels
                                                                                                                                                                                                                                                                                                                                                     391 LGFHSNNL-VASSWYYNNIRKNTSSNGCF------WSFI 422
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Best Local Similarity 31.5'
Matches 146; Conservative
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Search completed: March 2, 2006, 01:18:28 Job time : 18.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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; Search time 68.993 Seconds
(without alignments)
917.057 Million cell updates/sec 2, 2006, 00:31:42 March Run on:

US-08-981-087B-2
770
1 SYTNDKILLILYFNKLYKKIK......LNYNKIIWTLQDTAGNNQKL 144 Perfect score: Title:

**BLOSUM62** Scoring table: Sequence:

2443163 seqs, 439378781 residues Gapop 10.0 , Gapext 0.5 Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003s:\* geneseqp2003as:\* geneseqp2003bs:\* Geneseq 21:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:

#### SUMMARIES

		dР				
Result No.	Score	Query Match	Length	DB	ID	Description
	770	100.0	144	. ~	AAW09015	Aaw09015 Immunogen
8	770	100.0	431	~	AAW09014	Aaw09014 Immunogen
3	770	100.0	432	4	AAB04103	Aab04103 Botulism
4	770	100.0	432	4	AAB04096	Aab04096 Botulism
'n	770	100.0	645	4	AAE07894	Aae07894 Modified
ø	770	100.0	645	9	AAE35692	Aae35692 DipT HN d
7	770	100.0	657	9	AAE35693	Aae35693 BONT/F-Hc
80	770	100.0	657	9	AAE35694	Aae35694 BONT/F-Hc
σ	770	100.0	099	4	AAE07898	Aae07898 Modified
10	770	100.0	685	4	AAE07893	Aae07893 Modified
11	770	100.0	862	4	AAE07890	Aae07890 Modified
12	770	100.0	887	4	AAE07892	Aae07892 Modified
13	770	100.0	979	9	AAE35713	BO
14	770	100.0	1032	4	AAE07901	Aae07901 C. botuli
15	770	100.0	1059	ო	AAY93309	Aay93309 A mangane
16	770	100.0	1084	'n	AAY93312	A
17	770	100.0	1092	4	AAE07900	Aae07900 C. botuli
18	770	100.0	1192	ø	AAE35711	Aae35711 BONT/F-HC
19	770	100.0	1192	9	AAE35710	Aae35710 BONT/F-Hc
20	767	99.6	432	ო	AAY77138	Aay77138 Synthetic
21	593.5	77.1	448	~	AAW68399	Aaw68399 Clostridi
22	568.5	73.8	451	~	AAW68395	
23	565.5	73.4	449	m	AAY77137	Aay77137 Synthetic
24	565.5	73.4	449	4	AAB04094	Aab04094 Botulism

Aaw68396 Clostridi		Aay77140 Native bo	Aab04081 Botulism	Adz69764 Botulinum	_	Aay93310 A mangane	_	_	Adz36018 C. botuli	_	Adz69730 Botulinum	Adz69729 Clostridi	Adz69831 Inactive	Ad192142 Clostridi	Aau99339 Clostridi	Aay77143 Botulinum	Aay77142 Native bo	Aab04088 Botulism	Aar95008 Type A ne	Aaw68389 Clostridi
AAW68396	AAB04095	AAY77140	AAB04081	ADZ69764	AAY93307	AAY93310	AAR95010	ADW11038	ADZ36018	ADZ60275	ADZ69730	ADZ69729	ADZ69831	ADL92142	AAU99339	AAY77143	AAY77142 ·	AAB04088	AAR95008	AAW68389
2	9	17 3	7 4	6 69	17 3	3	96 2	6 9	6 9	6 9	6 96	9	9	8 8	5 5	33 3	432 3	437 4	438 2	438 2
4.	41	83.	84.	85	1067	1092	129	129	129	1296	129	130	13(	848	1295	23	4	4	4	4
72.9	8.69	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.0	48.4	48.2	48.2	48.2	48.2	48.2
561.5	537.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	377.5	372.5	371.5	371.5	371.5	371.5	371.5
25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism. Immunogenic type F botulinum toxin polypeptide (aa848-991). Pasechnik VA; Clostridium botulinum; type F strain Langeland Mauchline ML, Minton NP, (MICR-) MICROBIOLOGICAL RES AUTHORITY AAW09015 standard; protein; 144 AA. 95GB-00011909. (first entry) (revised) 12-JUN-1996; 12-JUN-1995; WO9641881-A1 27-DEC-1996. 17-OCT-2003 31-MAR-1997 Elmore MJ, AAW09015; AAW09015

WPI; 1997-065467/06.

Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.

Claim 5; Page 17-18; 37pp; English.

Novel polypeptides (AAM09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BoMT/F). They lack the L chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine produced Recombinant polypeptides can be produced in transformed host cells, as fusion proteins, e.g. with malcose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 144 AA;

Query Match

100.0%; Score 770; DB 2; Length 144;

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120

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infection
                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                     GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                       GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278) of a type F botulinum neurotowin (pown/p)
                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a type P botulinum neurotxin (BONT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                              1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                           1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                Gaps
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                                                                                                                                                                                                                                                                                                                                                                Immunogenic type F botulinum toxin heavy chain (aa848-1278).
                Indels
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100.0%; Pred. No. 1.7e-68;
ive 0; Mismatches 0;
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    Pred. No. 4.2e-69;
                                                                                                                                                                                                                                                                                                                                                                                                BoBT/F; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium botulinum; type F strain Langeland
                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elmore MJ, Mauchline ML, Minton NP,
                                                                                                                                                                                  121 WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                               121 WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 16-17; 37pp; English.
                                                                                                                                                                                                                                                                   AAW09014 standard, protein, 431 AA.
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100.08;
                                                                                                                                                                                                                                                                                                                                                                                                Botulinum toxin; neurotoxin;
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                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
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Best Local Similarity 100.
Matches 144; Conservative
                   Conservative
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N-PSDB; AAT48100.
   Best Local Similarity
Matches 144; Conserv
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                                                                                                                                                                                                                                                                                                                         17-OCT-2003
31-MAR-1997
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Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a condition heavy chain and a 50 kDa light chain which remain linked by a clisulfide bond. Nucleic acide encoding the carboxy-terminal (HC) or amino terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, thich causes botulism. The nucleic acide are expressible in a recombinant ocombinant nucleic acide are advantageous since it eliminates the need coupling the production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acide can be derived from the cost of production is lower. The nucleic acide can be derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                         61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                              Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith LA, Byrne MP, Middlebrook JL, Lapenotiere H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                      121 WKISLNYNKIIWTLQDTAGNNOKL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 18b; 73pp; English.
                                                                                                                                                                                           AAB04103 standard; protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0133865P.
99US-0133866P.
99US-0133867P.
99US-0133868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2000; 2000WO-US012890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0133873P
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-016048/02.
N-PSDB; AAA54499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against botulism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200067700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                             11-APR-2001
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12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000
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Score 770; DB 4; Length 432; Pred. No. 1.7e-68;

100.0%;

Query Match Best Local Similarity

Sequence 432 AA;

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Gaps

. 0

Indels

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SYTUDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF

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Clostridium botulinum serotypes A-G
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01-NOV-2001
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                                                                                                                                                                                                                                                                                                 AAE07894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric.
                                                 Query Match
                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                            AAE07894
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and then posttranslationally nicked, forming a dichain consisting of a

100 kDa heavy chain and a 50 kDa light chain which remain linked by a

disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino

terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT)

can be used in recombinant expression vectors and expressed in

transformed cells to produce peptide antigens useful for eliciting an

immune response to give protective immunity against botulinum neurotoxin,

which causes botulism. The nucleic acids are expressible in a recombinant

organisms such as Eschérichia coli or Pichia pastoris. The use of

recombinant nucleic acids are advantegeous since it aliminates the need

to culture large quantities of hazardous toxin-producing bacterium.

Production yield from the genetically engineered product is also high and

cost of production is lower. The nucleic acids can be derived from
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                                                                       GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                  9
                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      portions of
                                        2 SYTNDKILLLYFUKLYKKIKDNSILDDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                         1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
    Gaps
                                                                                                                                                                                                                                                                                                   Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
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0
                                                                                                                                                                                                                                                                            Botulism toxin heavy chain C-terminal sequence (serotype F)
    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Byrne MP, Middlebrook JL,
                                                                                                                                   122 WKISLNYNKIIWTLQDTAGNNQKL 145
                                                                                                                      WKISLNYNKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                         AAB04096 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 9b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0133866P.
99US-0133867P.
99US-0133868P.
99US-0133869P.
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                                                                                                                                                                                                                                                       (first entry)
      Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                               Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-016048/02.
N-PSDB; AAA54490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against botulism.
                                                                                                                                                                                                                                                                                                                                                                                     WO200067700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-2000;
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12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                    Synthetic
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours
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                                                                                                                                                                                                                                                                                                                  61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                         62 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIFKYFNKVNLNNBYTIIDCIRNNNSG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BoNT/F.
                                                                                                                                                                              0; Gaps
                                                       Length 432;
                                                                                                                         Indels
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                                                    100.0%; Score 770; DB 4;
100.0%; Pred. No. 1.7e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified clostridial heavy chain fragment #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKISLNYNKIIWTLQDTAGNNQKL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07894 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 44; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000; 2000WO-GB004644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                              Best Local Similarity 100.
Matches 144; Conservative
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Sequence 432 AA;
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   and infection. They are also useful in gene therapy. The present sequence is a modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain of botulinum neurotoxin type F (BONT/F) with translocation domain of diphtheria neurotoxin. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pumonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; translocation domain; HN domain; DipT; HC; botulinum type F neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                 215 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                     1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                      Length 645;
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100.0%; Pred. No. 2.9e-68;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE35692 standard; protein; 645
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Best Local Similarity 100.0
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding domain, BoNT/F.
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                                                                                                                                                                                               Sequence 645 AA;
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888688888
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for treatment selected from proming or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory

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mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular tracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating prion disease, Alzheimer disease and wide range of disorders inhibiting secretion disorders such as blephorospasm, torticolis and prion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and aschma. The present sequence is a fusion construct comprising Corynebacterium diphtheria diphtheria toxin translocation domain (Dip-HN domain) and botulinum type F neurotoxin from Clostridium botulinum. This sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; HC; binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                        1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                                                                                                                                                                        Length 645;
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 770; DB 6;
100.0%; Pred. No. 2.9e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 WKISLNYNKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 WKISLNYNKILWTLQDTAGNNQKL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2001; 2001GB-00012687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE35693 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium diphtheriae.
Clostridium botulinum.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     botulinum type F neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                     Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                Sequence 645 AA;
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                                                                                                                                                                                                                                                                                                                 Query Match
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(MICR-) MICROBIOLOGICAL RES AUTHORITY.

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287 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 346
                                                                                                                                                                                                                                                                                                                                                                   hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain), botulinum type F neurotoxin binding domain (BONT/F-Hc) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                  The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for the interfering expression of cell-surface markers and for the control of the control of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle appasm; CODP; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain;
                                                                                                                                                                                                                                                                                                    inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIVSTNRNQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 770; DB 6; Length 657; 100.0%; Pred. No. 3e-68; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BoNT/F-Hc-DipT HN domain-factor Xa linker fusion construct.
                Example 12; Page 60-63; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 WKISLNYNKIIWTLQDTAGNNQKL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE35694 standard; protein; 657 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           botulinum type F neurotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 657 AA;
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21-MAY-2002; 2002WO-GB002384. 24-MAY-2001; 2001GB-00012687.

WO200296467-A2.

05-DEC-2002

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory compliance from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell; for intracellular infection, for interfering with intracellular crafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for crafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for craticals grams such as blephorospasm, torticolis and including muscle spasms such as blephorospasm, torticolis and comprising corpusabacterium diphtheriae diphtheria toxin translocation comprising comprising corpusabacterium diphtheriae diphtheria toxin translocation comprising more comprising more comprising corpusabacterium diphtheriae diphtheria toxin translocation comprising corpus for construction of the invention general construction comprises the comprision of the invention of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 GIYSSKPSEVNIAQNNDIIYNGKYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 346
                                                                                                            LUNJUGATE TOT MODULATING CEll SURVIVAL AND CELL GROWTH, MODULATING release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; tetanus neurotoxin; TeNT; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 770; DB 6; Length 657; 100.0%; Pred. No. 3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified clostridial heavy chain fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                     Example 12; Page 63-65; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE07898 standard; protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium tetani.
Clostridium botulinum.
                                                                           WPI; 2003-167247/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 657 AA;
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01-NOV-2001
                                       Sutton JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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the invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructed and infection. They are also useful in gene therapy. The present sequence is and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain which is a hybrid of botulinum neurotoxin type F (BoNY/F) and tetanus neurotoxin (Updated on 11-SEP-2003 to translation) and the construction domain of diphtheria neurotoxin. (Updated on 11-SEP-2003 to
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                                                                                                                                                                                                                                                                                    New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIYSSKDSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBEYTIIDCIRNNNSG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; botulinum neurotoxin type F; BONI/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 46; 50pp; English.
                                                                                                                                                                                                              Silman N;
                                                                        04-DEC-2000; 2000WO-GB004644.
                                                                                                                                07-APR-2000; 2000GB-00008658
                                                                                                                99GB-00028530
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                                                                                                                                                                                                            Sutton JM,
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                                                                                                                                                                                                                                                WPI; 2001-514643/56.
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WO200158936-A2
                                                                                                                                                                                                                                                                                                        treatment of
                                                                                                            02-DEC-1999;
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                                      16-AUG-2001
                                                                                                                                                                                                            Shone CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
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Best Local
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HO) of a neurotoxin, designated as HO) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurocxin and is not a fragment or derivative of a HN domain of a clostridial neurocxin and is not a fragment or derivative of useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours
                                                                                                                                                                                                                                                                                                                                                                                                                 New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa, translocation peptide from influenza virus and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 SYTNDKILLIYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKISLNYNKIIWTLQDTAGNNOKL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Page 43; 50pp; English
                                                                                                                                                                                                                                                                                                                                         Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE07890 standard; protein; 862
Geobacillus stearothermophilus.
                                                                                                                                                                                                  04-DEC-2000; 2000WO-GB004644
                                                                                                                                                                                                                                       02-DEC-1999; 99GB-00028530
07-APR-2000; 2000GB-00008658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                    Influenza virus.
Clostridium botulinum.
Synthetic.
                                                                                                                                                                                                                                                                                                                                         Shone CC, Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514643/56.
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                                                                                                                   WO200158936-A2
                                                                                                                                                                                                                                     02-DEC-1999;
                                                                                                                                                           16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 144;
                                                                                Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE07890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ID AAE0
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AC AAE0
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DT 01-N
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314

AAE07892 standard, protein; 887 AA

(first entry)

01-NOV-2001

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (actorioxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the cost infection. They are also useful in gene therapy. The present sequence and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate compities bacterial hn-superoxide dismutase (MNSO), from the second conjugate of the conjug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                            Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 SYTNDKILILYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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Modified clostridial heavy chain-superoxide dismutase conjugate #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 862;
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100.0%; Pred. No. 4.2e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 WKISLNYNKIIWTLQDTAGNNOKL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silman N;
                                                                                                                                                                              Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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07-APR-2000; 2000GB-00008658.
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Best Local Similarity 100.
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-514643/56.
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                                                                                                                                                                                                                                                                                                                                           WO200158936-A2
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                                                                                                                                                                                                                                                                                         Chimeric
셤
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RESULT 12

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carboxy terminal half of heavy chain (HT) of a neurotoxin, designated as HC (carboxy terminal half of the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful to delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase (MmSOD), MnSOD from Bacillus steasortheramphilus, linker that can be cleaved by thrombin, translocation domain from diphtheria neurotoxin and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuronal cell; binding domain; translocation domain; stroke; epilepsy;
                                                                                                                                                   tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                                                                                                  Modified clostridial heavy chain-superoxide dismutase conjugate #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 770; D; 100.0%; Pred. No. 4.4. ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Page 42; 50pp; English.
                                                                                                                                                                                                                                            Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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07-APR-2000; 2000GB-00008658.
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Best Local Similarity 100.
Matches 144, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutton JM,
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                                                                                                                                                                                                                                                                                                                                                            40200158936-A2
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-2001
                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                          Chimeric.
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Sequence 979 AA;

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; contains the promoting or inhibiting survival of cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular mediator from cells, division of cells and treating intracellular infection and regulating mitric oxide release from cells. The invention cell, for intracellular infection, for interfering with intracellular cell, for intracellular infection of cell-surface markers and for trafficking, for modulating expression of cell-surface markers and for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spamms such as chronic obstructive pulmonary disease comprising corpression disorders such as chronic obstructive pulmonary disease comprising corpressorerium diphtheriae diphtheria toxin translocation comprising corpressorerium diphtheriae diphtheria toxin translocation (BONI/P-HC) from Clostridium botulinum and factor Xa linker peptide and Yersinia peetls targeted effector protein YopT. This sequence is used in the exemplification of the invention
Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; CODD, bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; Dipf; HC; binding domain; botulinum type F neurotoxin; targetted effector protien; YopT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Page 110-114; 130pp; English
                                                                                                                        WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                577 WKISLNYNKIIWTLQDTAGNNQKL 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAE35713 standard; protein; 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae Clostridium botulinum.
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                  RESULT 13
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is c. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BONT/F) binding domain used in the exemplification of
                                       ö
                                                                                                                                          120
                                                                                                       608
                                                                                                                                                        New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                      GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                  1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                          C. botulinum C2 translocation domain with BoNT/F-binding domain #2.
                                       ö
     Length 979;
                                     Indels
100.0%; Score 770; DB 6;
100.0%; Pred. No. 5e-68;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                          WKISLNYNKIIWTLQDTAGNNQKL 692
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                                                                                                                                                                                                                                                                                                                       AAE07901 standard; protein; 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2000; 2000WO-GB004644.
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07-APR-2000; 2000GB-00008658.
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton JM,
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                 Similarity
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                              Matches 144;
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Query Match
Best Local 8
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us-08-981-087b-2.rag

Sequence 1032 AA;

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GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG 120
                                                                                                                               1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                              Gaps
                              ;
0
100.0%; Score 770; DB 4; Length 1032; 100.0%; Pred. No. 5.4e-68;
                              Indels
                            0; Mismatches
                                                                                                                                                                         WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                     722 WKISLNYNKIIWTLQDTAGNNOKL 745
                               Matches 144; Conservative
                Best Local Similarity
                                                                                                                  61
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   Query Match
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Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                   A manganese superoxide dismutase (Mn-SOD) construct.
                                                    AAY93309 standard; protein; 1059 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Geobacillus stearothermophilus.
Clostridium botulinum.
                                                                                                                                                                              (first entry)
                                                                                                                                                                              04-SEP-2000
                                                                                                                AAY93309
RESULT 15
                            AAY93309
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(MICR-) MICROBIOLOGICAL RES AUTHORITY
             99WO-GB003699
                   98GB-00024282
WO200028041-A1
             05-NOV-1999;
                   05-NOV-1998;
      18-MAY-2000
```

Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia. WPI; 2000-376553/32.

Hallis B, Silman N;

Shone CC, Sutton JM,

Disclosure; Page 48-51; 65pp; English.

The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for heavy of SOD to neuronal cells. The composition comprises SOD linked, heavy clear the specification comprises SOD linked, heavy companies to the specification companies of SOD to neuronal cells. by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. "After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases

Sequence 1059 AA;

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                                                                                  629 SYTNDKILLIYENKLYKKIKDNSILDMRYENDISGYGSNISINGDVYIYSTNRNQF 688
                                                                                                                 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                  9
                                                       1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                             Gaps
                             ö
Length 1059;
                             Indels
100.0%; Score 770; DB 3; 100.0%; Pred. No. 5.5e-68;
                             0; Mismatches
                                                                                                                                                                               WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                749 WKISLNYNKIIWTLQDTAGNNQKL 772
   Query Match 100.
Best Local Similarity 100.
Matches 144; Conservative
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2, 2006, 00:38:55 Search completed: March Job time : 68.993 secs THIS PAGE BLANK (USPTO)

protein search, using sw model OM protein

March Run on:

2, 2006, 00:39:17 ; Search time 12.0278 Seconds (without alignments) 1151.928 Million cell updates/sec

US-08-981-087B-2 770 1 SYTNDKILILYFNKLYKKIK...........LNYNKIIWTLQDTAGNNQKL 144 score:

Title: Perfect ac Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

вишшагіев Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	neurotoxin type F	neurotoxin type F	neurotoxin type F	botulinum neurotox	neurotoxin type E	botulinum neurotox	botulinum neurotox	bontoxilysin (EC 3		bontoxilysin (EC 3	_	neurotoxin - Clost	botulinum neurotox	botulinum neurotox	botulinum neurotox	botulinum neurotox	tentoxilysin (EC 3	type E neurotoxin	botulinum toxin no	asparagine-rich bl	toxin, nontoxic co	botulinum neurotox	progenitor toxin n	botulinum neurotox	hypothetical prote	probable gtpase ac	nontoxic-nonhemagg	ORF MSV157 hypothe	nonstructural prot
ΩI	S48110	S48109	I40813	S33411	S48106	S21178	JH0256	BTCLAB	I40645	A48940	140631	S39791	A49777	S46431	\$11455	S70582	BICLIN	A53878	140817	B45600	JQ1467	S46430	A47708	868218	C82911	T38983	JC4901	T28318	MINVUMC
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Query Match Length	366	369	1274	1268	367	1252	1251	1296	1296	1291	1291	1297	1291	1291	1276	1285	1315	122	1162	480	1196	1196	1162	1193	457	743	1193	430	464
Query Match	100.0	81.4	81.4	81.2	74.2	74.2	73.8	49.2	49.0	46.1	45.2	41.4	32.5	32.5	32.4	31.7	26.8	26.1	16.2	15.2	14.9	14.9	14.8	14.7	14.5	14.5	14.3	13.6	13.1
Score	770	626.5	626.5	625	571.5	571.5	568.5	378.5	377.5	355	348	319	250	250	249.5	244	206	201	125	117	115	115	114	113	111.5	111.5	110	105	100.5
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C71609 JC6033 G71605	T10265 MNVUW1	S1,990 T28139 S72306	D71615 T18503	A71609 C64432	T28217 G90587	D71612 B64596
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# ALIGNMENTS

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neurotoxin type F - Clostridium botulinum (fragment)

neurotoxin type F - Clostridium botulinum

C;Species: Clostridium botulinum

C;Species: 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S48110

R;Campbell; K.D.; Collins, M.D.; East, A.K.

A;Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id

A;Accession: S48110

A;Residues: 1-366 <CAM>
A;Residues: 1-366 <CAM>
A;Cross-references: UNIPROT:057236; UNIPARC:UPI000016EA7C; EMBL:X70821; NID:g407792; PID
C;Superfamily: tetans toxin
C;Keywords: neurotoxin

ö Gaps ö Query Match 100.0%; Score 770; DB 2; Length 366; Best Local Similarity 100.0%; Pred. No. 3.5e-54; Matches 144; Conservative 0; Mismatches 0; Indels (

1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF

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В

61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 ò

유

121 WKISLNYNKIIWTLQDTAGNNOKL 144 ò 셤

334 WKISLNYNKIIWTLQDTAGNNOKL 357

#### RESULT S48109

neurotoxin type F - Clostridium botulinum (fragment) C;Species: Clostridium botulinum

C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 09-Jul-2004

C;Accession: S48109
R;Campbell, K.D.; Collins, M.D.; East, A.K.
A;Campbell, K.D.; Collins, M.D.; East, A.K.
A;Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48109

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-369 <CAM>

A;Cross-references: UNIPROT:P30996; UNIPARC:UPI000016EA7B; EMBL:X70820; NID:g407790; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 C;Superfamily: tetanus toxin

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Gaps

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61

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A;Molecule type: DNA
A;Residues: 1-1268 <THO>
A;Cross-references: UNIPROT:Q45851; UNIPARC:UPI0000BAF8C; EMBL:X68262; NID:g49138; PIDR
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                           900 IYSSRLSEVNITQNNTIINSRYQNFSVSFWVRIPKYNNLKALNNEYTIINCMRNNNSGW 959
                                                                                                                                                                                                                                                              2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKPIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                           840 YTNDKILIHILIRPYKRIIDSSILNMKYENNRFIDSSGYGSNISINGDIYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
                                                                                                                                                         Length 1268;
                                                                                                                                                                                                              Indels
                                                                                                                                                         Query Match 81.2%; Score 625; DB 2; L. Best Local Similarity 81.1%; Pred. No. 5.2e-42; Matches 116; Conservative 11; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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Best Local Similarity 71.7%; Pred. No. 2.3e-38;
Matches 104; Conservative 25; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurotoxin type E - Clostridium botulinum (fragment) C; Species: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GWKISLNYNKIIWTLQDTAGNNQKL 144
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A; Residues: 1-367 < CAM>
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A; Ascession: 140013
A; Ascession: 140013
A; Ascession: preliminary; translated from GB/EMBL/DDBJ
A; A; Calleule type: DNA
A; Chose-references: UNIPROT: P30996; UNIPARC: UP10000126B8A; GB: M92906; NID: G144866; PIDN: A; Cross-references: UNIPROT: P30996; UNIPARC: UP10000126B8A; GB: M92906; NID: G144866; PIDN: B; Campbell, K.D.; Collins, M.D.; Bast, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A; Ascession: S48108
A; Ascession: S48108
A; Status: preliminary; translation not shown
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A;Residues: 634-1002 <CAM>
A;Cross-references: UNIPARC:UPI00016EA7B; EMBL:X70816; NID:g407788; PIDN:CAAS0147.1; PI
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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botulinum neurotoxin type F - Clostridium barati
CjSpecies: Clostridium barati
CjSpecies: Clostridium barati
CjSpecies: Olostridium barati
CjAccession: 533411, 531860

R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.
FBMS Microbiol. Lett. 108, 175-182, 1933
A;Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin
A;Reference number: 533411; MUID:93252228; PMID:8486245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Clostridium botulinum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140813; S48108
R;East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, FEMS Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A;Reference number: 140644
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                                                                                                                                                            214 SYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQF 273
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       Length 369;
     Query Match 81.4%; Score 626.5; DB 2; Length 3 Best Local Similarity 80.3%; Pred. No. 9.6e-43; Matches 118; Conservative 14; Mismatches 12; Indels
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80.3%; Pred. No. 4e-42;
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neurotoxin type F - Clostridium botulinum
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C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 548106
R;Campbell, K.D; Collins, M.D.; Bast, A.K.
J. Cillins, Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cidence: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 31-Dec-2004
Cidencession: S21178; S48107; JH0257; B35294; A60027; S18111
Cidencession: S21178; S48107; JH0257; B35294; A60027; S18111
Bur. J. Biochem. 204, 657-667; 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxir A;Reference number: S21178; MUID:92174922; PMID:1541280
A;Accession: S21178
A;Accession: S21178
A;Residues: 1-1252 <WHE>
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q45861; UNIPARC:UPI00000B4F3D; EMBL.X70818; NID:g407784; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 C;Superfamily: tetanus toxin C;Superfamily: tetanus toxin C;Keywords: neurotoxin
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                                                                                                                                                                                                     A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48106
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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botulinum neurotoxin type E precursor - Clostridium botulinum
C;Species: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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PIL

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A; Experimental source: strains ATCC 43181 and ATCC 43755
R; Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N. C. Gen. Microbiol. 137, 519-525, 1991
A; Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxi. A; Reference number: S16145; MUID:91237316; PMID:2033376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: strain BL6340; Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lightware family: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 62A, subtype A R; Thompson, D.E.; Shone, C.C.; Atkinson, T R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T Bur, J. Biochem. 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin A; Reference number: S09492; MUID:90235864; PMID:2185020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1,'Q',3-26,'V',28-1296 <THO>
A;Cross-references:.UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-229,'M',231-252 <FUJ>
A;Cross-references: UNIPARC:UPI000016EA8F; EMBL;X53180; NID:g40407; PIDN:CAA37321.1; PID
A; Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type A; Reference number: JH0256; MUID:92181428; PMID:1543481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin component:
A,Reference number: S67988; MUID:96096783; PMID:8521962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1296 <BIN>
A;Cross-references: UNIPROT:P10845; UNIPARC:UPI000001386; GB:M30196; NID:g144864; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other
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NyAlternate names: botulinum neurotoxin type A
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T; Kurazono, H; Wille, M; Frevert, J; Wernars, K; Niemann, H.
J Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with A;Reference number: A35294; MUID:90264400; PMID:2160960
                                                                                                                                                                                                                                        EMBL: X62088; NID: 940379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                     A;Residues: 1-27,'E',29-1251 <POU>
A;Cross-references: UNIPROT:P30995; UNIPARC:UPI000017670D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.8%; Score 568.5; DB 2; Best Local Similarity 71.0%; Pred. No. 1.6e-37; Matches 103; Conservative 26; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
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                                                                                                                            A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GWKISLNYNKIIWTLODTAGNNOKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary Molecule type: DNA
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                                                                                             A:Accession: JH0256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S16145
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FEBS Lett. 37
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R;Gimenez, 1.A.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the si
A;Reference number: A60027; MUID:90344918; PMID:2116911
A;Reference number: A60027
A;Molecule type: protein
A;Residues: 420-427 <GIMA
A;Cression: A60027
A;Molecule type: protein
A;Residues: 420-427 <GIMA
A;Cression: A;Molecule type: protein
A;Residues: A10-427 <GIMA
A;Cression: A;Molecule type: protein Beluga
A;Molec: this fragment was generated by proteolysis with Lys-C rather than with trypsin
C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu-C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
C;Reywords: neurotoxin
F;1-422/Product: botulinum neurotoxin type E light chain #status predicted <LCH>F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>F;412-426/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                               Molecule type: DNA, Residues: 616-982 <CAM.
Residues: 616-982 <CAM.
Residues: 616-982 <CAM.
Residues: 616-982 <CAM.
Residues: 616-982 <CAM.
Residues: 616-982 <CAM.
Residues: UNIPARC:UPI00000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; PI
Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Foulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Foulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Fallite: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type
Reference number: JH0256; MUID:92181428; PMID:1543481
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Cross-references: UNIPARC:UPI000016EA7F; EMBL:X62089; NID:940393; PIDN:CAA43999.1; PID
                                                                                                                                   and specific id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         botulinum neurotoxin type A and comparison with other
                       .references: UNIPROT:Q00496; UNIPROT:Q45862; UNIPARC:UP100000010A3; EMBL:X62683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888
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R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
N. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparis.
A;Reference number: A35294; MUID:90264400; PMID:2160960
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                                  R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene A;Reference number: $48103; MUD:94013372; PMID:8408542
A;Accession: $48107
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R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R. Biochem. Biophys. Res. Commun. 183, 107-113, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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llarity 71.7%; Pred. No. 9.5e-38;
Conservative 25; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-176,'R',178-252 <BIN>
Cross-references: UNIPARC:UPI000017670F
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Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
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Dontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum

N;Alternate names: botulinum neurotoxin type B (BoNT/B)

C;Species: Clostridium botulinum

C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004

C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574

R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.

Appl. Environ. Microbiol. 58, 2345-2354, 1992

A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the ty:
A;Reference number: A48940; MUID:92384550; PMID:1514783
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A, Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this public.
R, Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262; 1995
A, Title: Gene probes for identification of the botulinal neurotoxin gene and specific in A, Reference number: $48103; MUID:94013372; PMID:8408542
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A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Cross-references: Unitabac: Up1000016EA7A; EMBL:X70817; NID:g407782; PIDN:CAAS0148.1; P
A; Experimental source: proteolytic type B, strain NCTC 7273
B; Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
R; Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
submitted to the EMBL Data Library, April 1992
A; Description: Partial amino acid sequence of botulinum neurotoxin type B and comparisis
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A;Residues: 36-217, 'G', 219-224, 'S', 226-246 <SZA>
A;Residues: 36-217, 'G', 219-224, 'S', 226-246 <SZA>
A;Cross-references: UNIPARC:UP1000016EA79; EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PII
R;Kurazono, H.; Mochida, S.; Binz, T.; Elsel, U.; Quanz, M.; Grebenstein, O.; Mernars, J. Biol. Chem. 267, 14721-14729, 1992
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A;Cross-references: UNIPROT:P10844; UNIPARC:UPI000016EA76; GB:M81186; NID:g144734; PIDN
                                                                                                                                                                                                                                                                                                                                                                    of Clostridium botulinum type
                                                                                                                         C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40645
R;Willems, A.; East, A.K.; Lawson, P.A.; Collins, M.D.
Res. Microbiol. 144, 547-556, 1993
A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A;Accession: I40645; MulD:94143603; PMID:8310180
A;Accession: I40645
A;Accession: I40645
A;Accession: I20645
A;Rocians preliminary; translated from GB/EMBL/DDBJ
A;Rosidues: 1-1296 «RES
A;Csession: UNIPROT:045894; UNIPARC:UPI000016EA88; EMBL:X73423; NID:g507070; C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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                                                                                             botulinum neurotoxin type A - Clostridium botulinum
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A; Status: preliminary
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A; Status: preliminary
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Best Local S
Matches 70
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A;Status: preliminary
A;Molecule type: protein
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A;Experimental source: strain Hall
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A;Experimental source: modified after ex
Biochimie 72, 661-664, 1990
A;Title: Datulinum neurotoxin type A: sequence of amino acids at the N-terminus and arou
A;Reference number: A60025; MUID:91120847; PMID:2126206
A;Accession: A60025
A;Molecule type: protein
A;Residues: 2-6;445-453, X', 455-457 cDAS1>
A;Cross-references: UNIPARC:UPI0000173658
A;Cross-references: UNIPARC:UPI0000173659
A;Cross-references: UNIPARC:UPI000173658
B;Dacdapta, B.R.; Folley, J: Niece, R.
B;Accession: A;Accession type A.
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPARC:UPI0000173655; EMBL:D67030; DDBJ:D50421; NID:g2160224
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A;Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term A;Reference number: A33401
A;Accession: A33401
A;Accession: A33401
A;Accession: A33401
A;Residuas: 1-35 < kBT>
A;Cross-references: UNIPARC:UPI000016EA84; GB:M27892; NID:g144880; PIDN:AAA23269.1; PID:R;Gimenaz, J.A.; DasGupta, B.R.
B;Gimenaz, J.A.; DasGupta, B.R.
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Arither Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A; Reference number: A49708; MUID:94124495; PMID:8294407
A; Contents: annotation
C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaptic comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaptic comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaptic serior:
A; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaptic serior:
A; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaptic seriorion:
A; Comment: Botulinum neurotoxins of an Asn-Arg peptide bond in synaptosomal-associate C; Function:
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A;Residues: 2-47 <DAS2>
A;Cross-references: UNIPARC:UP10000173659
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C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999.
C;Accession: S39791
R;Campbell, K.; Collins, M.D.; East, A.K.
Biochim. Biophys. Acta 1216, 487-491, 1993
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium A;Reference number: S39791; MUD:94092745; PMID:8268233
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Matches 67; Conservative
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C;Superfamily: tetanus toxin
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A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S48103
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A;Residues: 442-459 <$CH3>
A;Residues: 442-459 <$CH3>
A;Cross-references: UNIPARC:UPI0000173652
R;Cross-references: UNIPARC:UPI0000173652
Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt A;Reference number: $27125; MUID:93063293; PMID:1331807
A;Contents: annotation
A; Title: Minimal essential domains specifying toxicity of the light chains of tetanus to A; Reference number: A42871; MUID:92340509; PMID:1634516
A; Accession: A42871
A; Accession: A42871
A; Accession: A42871
A; Crase: Accession: A42871
A; Crase: Accession: A42871
A; Crase: Accession: A13, Cs. 315-451
A; Residues: 1-313, Cs. 315-451
A; Residues: 1-313, Cs. 315-451
A; Crose: Accession: A180000083742
A; Experimental Source: strain Okra
A; Note: sequence extracted from NCBI backbone (NCBIP:109365)
B; DasGupta, B.R.; Datta, A.
Biochimia 70, 811-817, 1988
A; Title: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A; Reference number: S07155; MUID:89000987; PMID:3139097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: bont/b
C;Function:
A;Gene: bont/b
C;Function:
A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
A;Descrimily: tetanus toxin
C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F;2-441/Product: bontoxilysin B light chain #status experimental <LGHT>
F;42-1291/Product: bontoxilysin B heavy chain #status experimental <HVY>
F;230,234/Binding site: zinc (His) #status predicted
F;231/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arch. Biochem. Biophys. 238, 544-548, 1985
A;Title: Partial amino acid sequences of botulinum neuro
A;Reference number: S07128; MUID:85197963; PMID:3888113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.1%; Score 355; DB 1; Le ilarity 47.3%; Pred. No. 1.7e-20; Conservative 33; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Readuse: 442-463,'R',465-467 <DA2>
A;Crose-references: UNIPARC:UPI0000173650
R;Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.
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Molecule type: protein
Residues: 2-16 <SCM1>
;Cross-references: UNIPARC:UP10000173652
                                                                                                                                                                                                                                                                                                                                                                              A,Accession: S07155
Modecule type: protein
A,Rediques: 2-29, M' 31-45 <DAS>
A,Cross-references: UNIPARC:UPI0000173650
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Residues: 2-17 <SCH2>
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Matches 69; Conserv
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140631; S48103; S48104; S36015
R;Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, D.B.
Curr. Microbiol. 28, 101-110, 1994
A;Title: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinum A;Reference number: 140631; MUD:94122659; PMID:7764370
A;Accession: 140631
A;Status: preliminary; translated from GB/EMBL/DDBJ
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. Clin. Microbiol. 31, 2255-2262, 1993
. Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
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A;Residues: 634-843, T',845, 'N',847-994 «CAM2»
A;Cross-references: UNIPARC:UPI00000B7A6E; EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PI
A;Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)
C;Comment: Botulinum neurotoxin type B in these strains may posses a capable catalytic s
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1, Residues: 634-761, E', 763-841,"M', 843,"T', 845,"N', 847-994 <CAM1>
1, CTOSS-references: UNIDARC: UPIO0000BEAEF; EMBL: X798 (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019) (1019
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Residues: 1-1291 <RES>
;Cross-references: UNIPROT:Q08077; UNIPARC:UPI0000BDC86; EMBL:X71343; NID:g296148;
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neurotoxin type B precursor - Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Status: preliminary; nucleic acid sequence not shown; translation not shown
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45.6%; Pred. No. 6.2e-20;
ive 35; Mismatches 39; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: S48103; MUID:94013372; PMID:8408542
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A;Residues: 1-1291 <HAU>
A;Cross.references: UNIPROT:Q93HT3; UNIPARC:UPI00000B3F60; EMBL:X72793; NID:g516171; PID
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A;Residues: 1-1276 <BIN>
A;Cross-references: UNIPROT:P19321; UNIPARC:UPI0000126B83; EMBL:X54254; NID:g40395; PIDNI
C;Superfamily: tetamus toxin
C;Keywords: neurotoxin
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Superfamily: tetanus toxin
                                                                                                                                       850 SYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIFPFDF 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doctulinum neurotoxin C1 - Clostridium botulinum phage IC (strain C 468)
NyAlternate names: BONT/C1 protein
Cispecies: Clostridium botulinum phage IC
Ayariety: strain C 468
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: 846431; 849107
Mol. Gen. Genet. 243, 631-640, 1994
A;Title: Organization of the botulinum neurotoxin C1 gene and its associated 1A;Reference number: 846426; MUID:94301293; PMID:8028579
A;Accession: 846431
A;Accession: Gaquence not shown; translation not shown
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium
C;Species: Clostridium
C;Accession: S1455
R;Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, Nucleic Acids Res. 18, 5556, 1990
A;Title: Nucleotide sequence of the gene encoding Clostridium botulinum neux
A;Reference number: S11455
A;Reference number: S11455
A;Reference number: S11455
A;Reference number: S11455
A;Reference number: S11455
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                                                                                                                                                                                                                                        119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
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| SGWSIGIISNFLVFTLKQNEDSEQSI 991
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Dotulinum neurotoxin type C1 precursor - Clostridium botulinum (type C, strain c-st)

C; Species: Clostridium botulinum
C; Species: Clostridium botulinum
C; Species: Clostridium botulinum
C; Species: Clostridium botulinum
C; Species: Clostridium botulinum
C; Species: D. Azise; Szle6; A49777

R; Hauser, D.; Eklund, M.W.; Kurazono, H.; Binz, T.; Niemann, H.; Gill, D.M.; Boquet, P.;
Nucleic Acids Res. 18, 4924, 1990

A; Ritle: Nucleotide sequence of Clostridium botulinum C1 neurotoxin.
A; Reference number: S11291; MUID: 90370487; PMID: 2204031

A; Residues: preliminary
A; Rocession: S1291
A; Residues: Leype: DNA
A; Residues: L' R' Pujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Takeshi, R.
Biochem: Biophys: Res. Commun. 171, 1304-1311, 1990
A; Rimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Takeshi, R.
Biochem: Biophys: Res. Commun. 171, 1304-1311, 1990
A; Reference number: A35396; MUID: 91024998; PMID: 2222445
A; Accession: A35396
A; Residues: L-669, R', 671-1291 <TSI
A; Residues: L-669, R', 671-1291
A; Residues: L-669, R', 771-1291
A; Residues: Residues: L-669, R', 771-1291
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A;Accession: $22166
A;Accession: $22166
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A;Accession: $22166
A;Accession: $22166
A;Residues: 1-1291 <TS2>
A;Residues: 1-1291 <TS2>
A;Crossareferences: UNIPARC:UPI00000B3F60; EMBL:X62389; NID:g558175; PIDN:CAA44263.1; PI R;Kimura; K.; Fujii, N.; Tsurauki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Oguma, K. Appl. Environ: Microbiol. 57, 1168-1172, 1991
A;Title: Cloning of the structural gene for Clostridium botulinum type C-1 toxin and who A;Reference number: A489777; MUID:91282468; PMID:2059039
A;Residues: 1-1297 <CAM>
A;Cross-references: UNIPARC:UPI0000176706; EMBL:X74162; NID:g441275; PIDN:CAA52275.1;
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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32.5%; Score 250; DB 2; Length 1291;
Best Local Similarity 37.7%; Pred. No. 4e-12;
Matches 55; Conservative 30; Mismatches 55; Indels
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41.4%; Score 319; DB 2;
Best Local Similarity 41.8%; Pred. No. 1.3e-17;
Matches 61; Conservative 26; Mismatches 55.
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C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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A;Molecule type: DNA
A;Residues: 1-607 <TS3>
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<sup>121</sup> WKISLNYNKIIWTLQDTAGNNQK 143 ||::|||||| 962 WKLCIRNGNIEWILQDV---NRK 981

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1375.940 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2166443 seqs, 705528306 residues
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058GH1 CLOBO
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Q54A79 CLOBO
BXE CLOBU
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Q57236_CLOBO
BXF_CLOBO
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Q9K395_CLOBU
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Listing first 45 summaries
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1 SYTNDKILILYFNKLYKKIK.
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2: uniprot_trembl:*
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Maximum DB
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999tg7 clostridium
P1931 clostridium
Q91br1 clostridium
Q95967 clostridium
Q958 clostridium
Q97107 clostridium
Q97101 clostridium
Q97101 clostridium
Q9501 clostridium
Q9501 clostridium
Q9501 clostridium
Q9501 clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWYRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campbell K.D., Collins M.D., East A.K.; "Gene probes for identification of the botulinal neurotoxin gene specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
Clostridium.
NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=type F;
Campbell K.D.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
366 AA; 43136 MW; 45A132B235D7E640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Botulinum neurotoxin type F (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 770; DB 2;
Pred. No. 4.8e-55;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               366
                 090TG7_CBDP
BXD_CLOBO
091ER1_CLOBO
045967_CLOBO
TETX_CLOTE
                                                                                                                                                             0985H1_CLOBO
045888_CLOBO
033871_CLOBO
092AJ9_CLOBO
P71117_CLOBO
                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X70821, CAA50152.1, -; Genomic_DNAHSSP, P04958; 1A8D.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                        CLOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                    09LA13
                                                                                                                                                                                                                                                                       006018
                                                                                                                                              Q93N27
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MEDLINE=94013372; Pubmed=8408542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; S
ilarity 100.0%; P
Conservative 0;
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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Q57236 CLOBO
ID Q57236_CLOBO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q79AH9 CLOBO PRELIMINARY;
Q79AH9;
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                                                           31.8
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079AH9

079AH9

AC 0793A

DT 0793AH9

DT 05-20

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OF 1-64.
  IDENTIFICATION OF SUBSTRATE.
  NUCLEOTIDE SEQUENCE
  HSSP; Q45894; 1E1H.
  MEROPS; M27.002;
  Lnum.
   removed.
ö
   848 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 907
   61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
   908 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 967
  9
   1 SYTNDKILILLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
  Gaps
   BONT/F (Neurotoxin type F).
Name=bont/f; Synonyms=bonT/F;
Clostridium botulinum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
  Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type P precursor (EC 3.4.24.69) (BoNT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain;
  ö
  Length 1278;
   Indels
  Elmore M.J., Bodsworth N.J., Whelan S.M., Minton N.P.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X81714; CAR57358.1; -; Genomic_DNA.
EMBL; L35496; AAA23210.1; -; Genomic_DNA.
  1278 AA; 147073 MW; AIBE1318431D6918 CRC64;
  Hutson R.A., Collins M.D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
  HSSP, Q45694; IEIH.
MEROPS; M27.002; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:000508; P:pathogenesis; IEA.
            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
  100.0%; Score 770; DB 2;
100.0%; Pred. No. 1.8e-54;
ive 0; Mismatches 0;
   InterPro; IPR011591; Botulinum.
InterPro; IPR001395; Peptidase_M27.
InterPro; IPR006025; Peptidase_M27.
Pfam, PF01742; Peptidase_M27; I.
PR107760; BONTOXILYSIN.
ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
   1274 AA
   968 WKISLNYNKIIWTLQDTAGNNQKL 991
   WKISLNYNKIIWTLQDTAGNNOKL 144
  Botulinum neurotoxin F heavy chain]
  Matches 144; Conservative
  STANDARD;
   Clostridium botulinum
  NUCLEOTIDE SEQUENCE.
   NUCLEOTIDE SEQUENCE
  NUCLEOTIDE SEQUENCE.
  Local Similarity
  STRAIN-NCTC 10281;
   NCBI_TaxID=1491;
  Clostridium.
NCBI_TaxID=1491;
  Neurotoxin.
  CLOBO
  SEQUENCE
  121
   Query Match
  BXF_CLOBO
  RESULT 3
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STRAIN=Type F / ATCC 23387;

DO DE BOUNDE BY SERVICE ```
MEDLINE=94230352; PubMed=8175689;

MEDLINE=94230352; PubMed=8175689;

RA Famasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F.,

RA Pamasaki S., Baumeister A., Binz T., Jahn R., Niemann H.;

Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;

R. "Cleavage of members of the synaptobrevin/VaMP family by types D and F potulinal neurocoxins and tetanus toxin.";

J. Biol. Chem. 269:12764-12772(1994).

C. FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter celease. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-59 bond of synaptobrevins-1 and -2.

C.-I. CAPALYITIC ACTIVITY: Linited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

C.-I. COFACIOR: Binds 1 zinc ion per subunit (By similarity).

C.-I. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94013372; PubMed=8408542; Campbell K.D., Collins M.D., East A.K.; Gampbell K.D., Collins M.D., East A.K.; "Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Type F / Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
East A.K., Collins M.D.;
"Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic Clostridium botulinum type F.";
MEDLINE=93012902; PubMed=1398040; DOI=10.1016/0378-1097(92)90408-G; East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A., Thompson D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      formation and toxin binding, respectively.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANBOUGS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
-!- SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                      'Sequence of the gene encoding type F neurotoxin of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M92906; AAA23263.1; -; Genomic_DNA.

EMBL; S73676; AAC60475.1; -; Genomic_DNA.

EMBL; X70820; CAA50151.1; -; Genomic_DNA.

EMBL; X70816; CAA50147.1; -; Genomic_DNA.

PIR; 140813; 140813.
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InterPro; IPR00159; Pept M Zn BS.
InterPro; IPR00195; Pept M Zn BS.
InterPro; IPR012928; Toxin recpt bd.N.
InterPro; IPR012928; Toxin recpt bd.N.
InterPro; IPR012500; Toxin trans.
Pfam; PF07742; Peptidase MZ7; 1.
Pfam; PF07952; Toxin R bind N; 1.
Pfam; PR07952; Toxin trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease;
Toxin; Transmembrane; Zinc.
                                                                                                                   Botulinum neurotoxin F light chain.
Botulinum neurotoxin F heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy
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                                                                                                                                                                                                                                                                                                                                                                       81.4%; Score 626.5; DB 1; Length 80.3%; Pred. No. 1.1e-42; ive 14; Mismatches 12; Indels
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PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1280 AA; 147486 MW; D0F748976EBC222C CRC64;
                                                                                                                                                                                                                                                                                          chains) (Probable).
1274 AA; 146710 MW; 5B99756A7438B921 CRC64;
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Santos-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y13631; CAA73972.1; -; Genomic_DNA.
HSSP; Q45894; IEIH.
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Last annotation update)
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InterPro; IPR000395; Peptidase MZ7.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PF01742; Peptidase MZ7; 1.
PRINTS; PR00760; BONTOXILYSIN.
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Matches 118; Conservative
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STRAIN-CDC 3281;
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ACT SITE
METAL
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DISULPID
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PEMS Microbiol. Lett. 108:175-182(1993).

EMBL; X68262; CAA48329.1; -; Genomic_DNA.

PIR; S33411; S33411.
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BENDINES-3152228; PubMed=8486245; DOI=10.1016/0378-1097(93)90581-L;

Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,

Richardson P.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Length 1280;
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                                               Indels
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR001395; Peptidase_M27.
InterPro; IPR006025; Peptidase_M27.
FRIM; PR01747; Peptidase_M27; IPRN0780; BONTOXILYSIN.
ProDom; P001963; Botulinum; I.
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Last annotation update)
  81.2%; Score 625.5; DB 2;
80.3%; Pred. No. 1.3e-42;
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Neurotoxin.
                              , Pred. No. 1.3e
13; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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Matches 116; Conservative
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Q45851;
                              Best Local Similarity 80.3
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurotoxin type F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=bont /f;
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us-08-981-087b-2.rup

045861

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STRAIN=ATCC 43181, and ATCC 43755;
MEDLINE=92181428; PubMed=1543481;
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                       1252 AA; 143637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 1-251.
                                                                                                                   Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 1-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium butyricum.
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                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1492;
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Neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BXE CLOBU
                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                    949
                         SEQUENCE
                                                                     Query Match
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BXE_CLOBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 GIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVNVNNEYTIINCMRDNNS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Campbell K.D., Collins M.D., East A.K., "Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
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TBUKamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T., Nakamura S., Karasawa T., Kozaki S., Samura S., Karasawa T., Kozaki S., Sequence of the botulinum neurotoxin type E.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
                                                                                                                                                                                                   Clostridium botulinum.
Bacteria, Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium botulinum.
Bacteriai, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 367
367 AA; 42902 MW; 346A610C2FF70262 CRC64;
                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurocoxin type E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X70818; CAA50149.1; -; Genomic_DNAPIR; S48106; S48106.
                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequer
01-OCT-2003 (TrEMBLrel. 25, Last annote
Botulinum neurotoxin type E (Fragment).
Name=BONT/E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 GWKVSLNHNEIIWTLQDNAGINQKL 358
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P10844; 1F31.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GWKISLNYNKIIWTLODTAGNNOKL
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94013372; PubMed=8408542;
                         Q45861_CLOBO PRELIMINARY;
Q45861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q54A79 CLOBO PRELIMINARY;
Q54A79;
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                      NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=type E;
Campbell K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotoxin.
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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               CLOBO
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Matches 10
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"Neurotoxin type E from Clostridium botulinum and C. butyricum;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";

FASEB J. 2.41750-41750(1988).
-!- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter
release. It binds to peripheral neuronal synapses, is internalized
and moves by retrograde transport up the axon into the spinal cord
where it can move between postsynaptic and presynaptic neurons. It
inhibits neurotransmitter release by acting as a zinc
                                                                                                                                                                                                                                                         endopeptidase.
CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
                                                                                                                                                                                                               1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                             61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loning of a DNA fragment encoding the 5'-terminus of the botulinum pe E toxin gene from Clostridium butyricum strain BL6340."; Gen. Microbiol. 137:519-525(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755)."; Biochem. Biophys. Res. Commun. 183:107-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BONT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
Botulinum neurotoxin E heavy chain]
                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                        Length 1252;
                                                                                                                                              Indels
76401D4D2E95D7A2 CRC64;
                                                                 74.2%; Score 571.5; DB 2; 71.7%; Pred. No. 3.3e-38; ive 25; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1250 AA
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1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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Wang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
Genetic analysis of type B botulinum toxin-producing Clostridium
butyricum strains.";
Appl. Environ. Microbiol. 66:4992-4997 (2000).
Embl., AB019264; BAB12249.1; -; Genomic_DNA.
           TSUKAMOTO K., MUKAMOTO M., Kohda T., Ihara H., Wang X., Maegawa T., Nakamura S., Karasawa T., Kozaki S.;
Submitted (ULL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BAG08207; BAC05434.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.8%; Score 568.5; DB 2; Length 1252; 71.0%; Pred. No. 5.9e-38; ive 26; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41B633BB744D3B41 CRC64;
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GO; GO:001621; C:integral to membrane; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR010591; Boculinum.
InterPro; IPR000395; Peptidase_M27.
InterPro; IPR006025; Pept M Zn_BS.
Pfam; PF01742; Peptidase_M27; I.
PRINTS; PR00760; BONTOXILIYSIN.
ProDom; PD001963; Botulinum; 1.
                                                                                                                                                                             GO; GO: 001621; C:integral to membrane; IEA.
GO; GO: 001621; C:integral to membrane; IEA.
GO; GO: 0008237; F:metallopeptidase activity; IEA.
GO; GO: 0008208; F:prathogenesis; IEA.
GO; GO: 0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR00135; Peptidase M27.
InterPro; IPR00035; Peptidase M27.
InterPro; IPR006025; Pept M Zn_BS.
Ffam; PP01742; Peptidase M27; I.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; BOULInum; 1.
PROSITE; PS00142; ZINC PROTEARS; UNKNOWN I.
SEQUENCE 1252 AA; 143510 MW; 41B633BB744D3B41 CRC64
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Last annotation update)
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MEDLINE=20509829; PubMed=11055954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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16,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.0%;
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Q9FAR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.0%,
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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                                                                                                                                    HSSP; Q45894
SMR; Q8KZM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=bont/E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMR; Q9FAR6;
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Q9FAR6 CLOBU
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                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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R InterPro; IPR006025; Pept M_Zn_BS.
R InterPro; IPR006025; Pept M_Zn_BS.
R InterPro; IPR0012928; Toxin_recpt_bd_N.
R InterPro; IPR012929; Toxin_recpt_bd_N.
R InterPro; IPR012929; Toxin_trans.
R Pfam; PP07953; Toxin_trans.
R Pfam; PP07953; Toxin_trans.
R Pfam; PP07952; Toxin_trans.
R Pfam; PR001960; BONTOXILYSIN.
R PRNTS; PR001961; BOULININN; 1.
R PROSITE; PS00142; ZINC_PR0TEASE; 1.
N Neutocom; Protease; Toxin; Transmembrane; Zinc.
M Neutocoxin; Protease; Toxin; Transmembrane; Zinc.
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                          MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
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215 215 Zinc (catalytic) (By similarity).
411 425 Interchain (between light and heavy catalys).
229 229 K -> M (in Ref. 2).
1250 AA; 143266 MW; 8171B5B2C2312857 CRC64;
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Botulinum neurotoxin E heavy chain.
By similarity
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EMBL; X53180; CAA37321.1; -; Genomic_DNA.
PIR; JH0256; JH0256.
PIR; JH0256; JH0256.
SMR; P30995; 1.411.
MEROPS; M27.002; -
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QBKZM3;
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Clostridium.
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                                                                               Length 1255;
300142; ZINC_PROTEASE; UNKNOWN 1.
1255 AA; 143917 MW; 1B557B9DB5CDBE4D CRC64;
                                                                                                                                 Indels
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2021F4E427070296 CRC64;
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GO; GO:0008405; F:peptidase activity; IEA.
GO; GO:0008405; F:perceolysis and peptidolysis; IEA.
GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
InterPro; IPR011591; Botulium.
InterPro; IPR01291; Peptidase M27.
InterPro; IPR01298; Poxin_recpt_bd_N.
InterPro; IPR01298; Toxin_recpt_bd_N.
InterPro; IPR012500; Toxin_recpt_bd_N.
InterPro; IPR012500; Toxin_respt_bd_N.
IPR01781; PR01782; Toxin_respt_bd_N.
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                                                                               DB 2;
                                                                       13.8%; Score 568.5; DB 2 ilarity 71.0%; Pred. No. 5.9e-38; Conservative 26; Mismatches 15
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EMBL; AB0377106; BAE03514.1; -; Genomic_DNA.
EMBL; AB037712; BAE03518.1; -; Genomic_DNA.
EMBL; AB037712; BAE03520.1; -; Genomic_DNA.
EMBL; AB037713; BAE03521.1; -; Genomic_DNA.
EMBL; AB037713; BAE03521.1; -; Genomic_DNA.
EMBL; AB037709; BAE0351.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                               952 GWKVSLNHNEIIWTLQDNSGINQKL 976
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Q9K395,
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     PS00142;
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PROSITE; I
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                              829 SYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGEIFIYPTNKNOF
                                                                                                                                                                                                                                                                                                                                    1 SYTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                              61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS
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                                                                                Gaps
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Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;

"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
J. Biol. Chem. 265:9153-9158(1990).
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MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755)...;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BONT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
                                                                            1;
       Length 1251;
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                                                                        Indels
Query Match 73.3%; Score 564.5; DB 2; Best Local Similarity 69.7%; Pred. No. 1.3e-37; Matches 101; Conservative 29; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GWKISLNYNKIIWTLQDTAGNNOKL 144
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MEDLINE=94013372; Pubmed=8408542;
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PROTEIN SEQUENCE OF 419-426
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MEDILIBE-94124495; PubMed-8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
A Jahn R., Mismann H.;
John R., Mismann H.;
John R., Mismann H.;
J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

I. FUNCTION: Boculinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc inhibiting neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 180-Arg-|-11e-corporation of the spinal cord and in SNAP-25.

J. CAPTALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

J. COFACTOR: Binds 1 zinc ion per subunit (By similarity).

J. SUBUNIT: Disulfide-linked heterodimer of a light chain (I) and a heavy chain (II). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ruropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                         neurotoxin gene and
                                                                                                               IDENTIFICATION OF SUBSTRATE.

MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Bottenati F., Wilson M.C., Montecucco C.; COH-terminal peptide bonds "s. Petilona neurotoxins serotypes A and E cleave SNAP-25 at distinct PERS Lett. 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                formation and toxin binding, respectively.
SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
SIMILARITY: Belongs to the peptidase M27 family.
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Botulinum neurotoxin E heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy
  Campbell K.D., Colling M.D., East A.K.;
Gene probes for identification of the botulinal neurotoxin
specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X62089; CAA4399.1; -; Genomic_DNA.
EMBL; X62683; CAA44558.1; -; Genomic_DNA.
EMBL; X70815; CAA50146.1; -; Genomic_DNA.
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InterPro; IPR001625; Pept M Zn BS.
InterPro; IPR000395; Peptidase_M27.
InterPro; IPR012928; Toxin_recpt_bd_N.
InterPro; IPR012828; Toxin_trans.
Pfam; PP01742; Peptidase_M27; 1.
Pfam; PP07953; Toxin_R bind_N; 1.
Pfam; PP07952; Toxin_trans; 1.
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ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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PIR; S21178; S21178.
PDB; 1T3A; X-ray; A/B=1-421.
PDB; 1T3C; X-ray; A/B=1-421.
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MBDINE=97016817; PubMed=8863443;
BEST A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
Esst A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
Granization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
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MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
with complete sequence of bottlinum neurotoxin type A and comparison
with other clostridial neurotoxins.";
J. Biol. Chem. 265:9153-9158(1990).
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"The complete amino acid sequence of the Clostridium botulinum type neurotoxin, deduced by nucleotide sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P10845; P01561; P18639; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 26, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A) (Bontoxilysin A) (BOTOX) (Contains: Botulinum neurotoxin A light-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                         Length 1250;
                 176 R -> G (in Ref. 2).
197 C -> S (in Ref. 2 and 3).
339 R -> A (in Ref. 2).
772 I -> LQ (in Ref. 2 and 6).
963 FE -> LQ (in Ref. 2 and 6).
964 R -> A (in Ref. 2 and 6).
194 N -> N (in Ref. 2 and 6).
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                                                                                                                                                                                                                   D9FCE26DDA041EB4 CRC64;
                                                                                                                                                                                                                                                                   ; Score 559.5; DB 1;
; Pred. No. 3.2e-37;
26; Mismatches 17;
(Probable).
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chains)
R -> G (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Type A / NCTC 2916;
MEDLINE=90235864; Pubmed=2185020;
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NUCLEOTIDE SEQUENCE OF 1-34.
STRAIN=TYPE A / Hall;
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339
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MEDLINE=85285016; PubMed=3896784; Shone C.C., Hambleton P., Melling J.; Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity."; Eur. J. Blochem. 151:75-82(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dasgupta B.R., Foley J., Niece R., "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
                                                                                                                                                STRAIN=TYPE A / NIH;
MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(95)01241-5;
MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(95)01241-5;
Fujita R., Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.;
"Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins.";
                                            of
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Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Niemann H., Yamasaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Miemann H., Yamasaki S., Yamasaki S., Baumeister S., Jahn R., Jahn S.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [12]
IDENTIFICATION OF SUBSTRATE.
MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4;
Schlavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J.,
Benfenati F., Wilson M.C., Montecucco C.;
"Botulinum neurocoxins serocypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bons.";
              Betley M.J., Somers E., Dasgupta B.R.; "Characterization of botulinum type A neurotoxin gene: delineation the N-terminal encoding region."; Biochem. Biophys. Res. Commun. 162:1388-1395(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91120847; PubMed=2126206; DOI=10.1016/0300-9084(90)90048-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE C. MANAGE 1178218; MEDLINE=89024662; PubMed=1178218; Sathymostrhy V., Dasgupta B.R., Foley J., Niece R.L.; Sathymostrhy V., Dasgupta B.R., Foley J., Niece R.L.; Botulinum neurotoxin type A: cleavage of the heavy chain into two "Botulinum neurotoxin type A: cleavage of the heavy chain into two """"" and their partial sequences.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gimenez J.A., DasGupta B.R.; Botulinum type A neurotoxin digested with pepsin yields 132, 97, 45, 42, and 18 M fragments 1. Protein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dasgupta B.R., Dekleva M.L.; "Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site."; Biochimie 72:661-664(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
                                                                                                                                                                                                                                                                                                                                                           Schmidt J.J., Sartymoorthy V., Dasgupta B.R.; "Partial amino acid sequence of the heavy and light chains of
                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 119:900-904(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE OF 448-474 AND 872-895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 1-5 AND 444-456.
MEDLINE=89350959; PubMed=2669749;
                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 1-16.
MEDLINE=84178501; Pubmed=6370252;
                                                                                                                                                                                                                                                                                                                                                                                                            neurotoxin type A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 448-482.
                                                                                                                                 NUCLEOTIDE SEQUENCE OF 1-18.
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                                                                                                                                                                                                                                                                   Lett. 376:41-44(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 1-46.
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                                                                                                                                                                                                                                                                                                                                                                                                            botulinum
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                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Inhibits acceptional release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

-i- MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
-i- SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                           MEDLINE=98455071; PubMed=9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

COPACTOR: Binds 1 zinc ion per subunit.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWW="http://www.botox.com/site/".
DATABASE: NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      results in flaccid paralysis, with frequent heart or respiratory
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"Site-directed mutagenesis identifies active-site residues of the light chain of botulinum neurotoxin type a."; Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
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Botulinum neurotoxin A heavy-chain.
Potential.
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PROSITE; PS00142; ZINC_PROTEASE; I.
3D-etructure; Direct protein sequencing; Hydrolase; Metal-binc Metalloprotes; Neurotoxin; Pharmaceutical; Protease; Toxin; Transmembrane; Zinc.
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EMBL; M30196; AAA23262.1; -; Genomic_DNA.
EMBL; X92973; CAA63551.1; -; Genomic_DNA.
EMBL; D67030; BAA11051.1; -; Genomic_DNA.
EMBL; M27892; AAA23269.1; -; Genomic_DNA.
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006035; Pept M Zn BS.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012500; Toxin rerans.
Pfam; PF01742; Peptidase M77; 1.
Pfam; PF07953; Toxin R bind N; 1.
Pfam; PF07952; Toxin R bind N; 1.
Pfam; PF07952; Toxin Lrans; 1.
                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                  toxicity.";
Nat. Struct. Biol. 5:898-902(1998)
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PDB; 3BTA; X-ray; A=1-1295.
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STRAIN=Allergan-Hall A;
STRAIN=Allergan-Hall A;
MEDLINE=22919384; PubMed=14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zhang L., Lin W.J., Li S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
Clostridium botulinum type A-Hall (Allergan) strain.";
Gene 315:21-32(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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"Neurotoxin gene clusters in Clostridium botulinum type A strains:
sequence comparison and evolutionary implications.";
Curr. Microbiol. 46:345-352(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Hall A-hyper;
MEDLINE=22617869; PubMed=12732962; DOI=10.1007/800284-002-3851-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                               Interchain (between light and heavy chains).
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Last annotation update)
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                                                                          (catalytic)
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EMBL; AF488749; AAQ06331.1; -; Genomic_DNA.
Potential.
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Best Local Similarity
Matches 69; Conserv;
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The Crterminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus adherence of the toxin to the cell surface while the N-terminus adherence of the toxin to the cell surface while the N-terminus adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure (By similarity).

GARALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevine, SNAP25 or syntaxin. No
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MEDLINE=97016817; PubMed=8863443;

Rast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

Rast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

Camponents of the botulinum toxin complex in proteolytic Clostridium botulinum types A. B. and P. evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";

Jin. J. Syst. Bacteriol. 46:1105-1112(1996).

--- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Type A / Kyoto-F;
MEDLINE=94143603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
Willems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridium
botulinum type A associated with infant botulism: comparison with
other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroexocytosis apparatus, synapcobrevins, SNAP25 or syntaxin. detected action on small molecule substrates. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain (H) (By similarity).
SUBCELLULAR LOCATION: Secréted.
MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
(Boncoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain]
                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                   PRT; 1295 AA.
122 KISLNYNKIIWTLODTAGNNOKL 144
                         Name=botA; Synonyms=atx, bna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 1-65.
                                                                                                                                                     STANDARD;
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                                                                                                                                                   BXA2 CLOBO (045894; P77780;
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BXA2_CLOBO
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EMBL; X73423; CAA51824.1; -; Genomic\_DNA. EBMB; X87974; CAA61234.1; -; Genomic\_DNA. PIR; 140645; 140645. PDB; 1EIH; X-ray; A/C=9-249; B/D=250-415.

removed

MBROPS; M27.002; -. InterPro; IPR011591; Botulinum.

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2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKPIDISGYGSNISINGDVYIYSTNRNQFG 61
R InterPro; IPR006025; Pept_M Zn_BS.
R InterPro; IPR00395; Peptidase M27.
R InterPro; IPR012928; Toxin_recpt_bd_N.
InterPro; IPR012509; Toxin_recpt_bd_N.
R InterPro; IPR012509; Toxin_rene.
R Pfam; PF01742; Peptidase M27; 1.
R Pfam; PF07953; Toxin_trans; 1.
R Pfam; PF07953; Toxin_trans; 1.
R Pfam; PF07953; Toxin_trans; 1.
R PRINTS; PR00760; BONTOXILYSIN.
R PROSUTE; PS00142; ZINC_PF07EASE; FALSE_NEG.
N 3D-structure; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin;
N Protease; Toxin; Transmembrane; Zinc.
R Protease; Toxin; Transmembrane; Zinc.
THAIN 1 40 Botulinum neurotoxin A light-chain.
THAIN 448 1295 Botulinum neurotoxin A heavy-chain.
                                                                                                                                                                                                                                                626 646 Potential.
625 675 Potential.
223 222 Zinc (catalytic) (By similarity).
226 226 Zinc (catalytic) (By similarity).
429 453 Interchain (between light and heavy channs) (By similarity).
1234 1279 By similarity.
1295 AA; 149280 MW; 5DA04Al3D98D6372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.0%; Score 377.5; DB 1; Length 1295;
Best Local Similarity 49.0%; Pred. No. 2.8e-22;
Matches 70; Conservative 29; Mismatches 43; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 KISLNYNKIIWTLODTAGNNOKL 144
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Search completed: March 2, 2006, 00:46:24 Job time : 74.8376 secs

Sequence Sequence Sequence Sequence

Sequence

Sequence Seq

OM protein

Run on:

Sequence:

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| Sequence 28, Application US/08480604A
| Patent No. 5736139
| GENERAL INPORMATION:
| APPLICANT: KINK, JOHN A.
| APPLICANT: PADHYE, NISHA V.
| APPLICANT: PADHYE, NISHA V.
| APPLICANT: STAFFORD, DOUGLAS C.
| TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: ADDRESSE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
OPERATING SYSTEM:
OURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 16-AAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/426,496
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
FILING DATE: 10-DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FRIUNG DATE: 04-DEC-1992
FRIUNG DATE: 31-OCT-1992
FRIUNG DATE: 31-OCT-1992
FRIUNG DATA:
APPLICATION NUMBER: US 07/429,791
FRIUNG DATE: 31-OCT-1992
FRIUNG DATE: 10-DEC-1992
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US-08-158-9
US-08-446-855A-2
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US-09-079-030-214
US-09-108-006C-1
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US-09-134-001C-2993
US-09-134-001C-2993
US-08-134-001C-2993
US-08-134-001C-2993
US-08-687B-30
US-09-662-254B-20
US-09-662-254B-20
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STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                        March 2, 2006, 00:46:47; Search time 17.7077 Seconds (without alignments) 672.325 Million cell updates/sec
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1 SYTNDKILILYFNKLYKKIK.........LNYNKIIWTLQDTAGNNQKL 144
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                        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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S-09-084-517-28
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S-08-480-604A-23
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match
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Perfect score:
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Minimum DB Maximum DB

Searched:

Database :

Result

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                                                                                                                                                                                                                                                                 Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                         42; Indels
                                                                                                                                                                                                                                                      49.2%; Score 378.5; DB 1;
48.3%; Pred. No. 5.8e-31;
tive 31; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A FILING DATE: 16 MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTONEY FARMATION:
NAME: INGOLIA, DIANE E:
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
REFERENCE/DOCKET NUMBER: OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 KISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         975 KVSLNYGEIIWTLQDTQEIKQRV 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94104
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.31
Matches 69; Conservative
                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                              US-08-480-604A-28
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                                                                                                                                                                                                                         Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, USHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTIONS: 32
CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                      DB 1;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
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49.2%; Score 378.5; DB 1
Best Local Similarity 48.3%; Pred. No. 5.8e-31;
Matches 69; Conservative 31; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN PRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
FILING DATE:
PRIOR APPLICATION NUMBER: 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 KISLNYNKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 975 KVSLNYGEIIWTLQDTQEIKQRV 997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08915136
Patent No. 6290960
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                     TOPOLOGY: linear; MOLECULE TYPE: protein US-08-405-496A-28
                                                                                     amino acid
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CARROLL, PETER G.
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US-08-480-604A-23
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                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                             2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKPIDISGYGSNISINGDVYIYSTNRNOFG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09084517
| Patent No. 661329
| GENERAL INFORMATION
| APPLICANT: WILLIAMS, JAMES A. |
| APPLICANT: WILLIAMS, JAMES A. |
| TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: 30
| CORRESPONDENCE ADDRESS: 30
| STREET: 220 MONTGOMERY STREET, SUITE 2200
| STREET: SAN FRANCISCO STATE: CALIFORNIA STATE: COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                            DB 2; Length 1296;
                                                                                                                                                                                                                                                                                                 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRIT DATED STATES OF PUBLICAL
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version. #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                          ch 49.2%; Score 378.5; DB 2
1 Similarity 48.3%; Pred. No. 5.8e-31;
69; Conservative 31; Mismatches 42
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR AND CATES OF COLUMN PRINCIPLE APPLICATION DATA:
APRLICATION NUMBER: US 07/965,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US 08/161,907
02-DEC-1993
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                                                                                                                                                                                               / MOLECULE TYPE: protein US-08-915-136-28
                                                                                                                                                                      amino acid
                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                     TOPOLOGY:
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Sequence 219, Application US/10360101

Sequence 219, Application US/10360101

Sequence 219, Application US/10360101

Patcht No. 6861236

GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way FILE REFERENCE: 2103-5673

CURRENT APPLICATION NUMBER: US/10/360,101

CURRENT APPLICATION NUMBER: EP 02077060.8

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

SOFTWARE: Patchtln version 3.1

SEQ ID NO 219

LENGTH: 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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Best Local Similarity 49.0%; Pred. No. 4.2e-31;
Matches 70; Conservative 29; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.2%; Score 378.5; DB 2 ilarity 48.3%; Pred. No. 5.8e-31; Conservative 31; Mismatches 42
                                                           OPHD-01610
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                           TELEPHONE: (415) 705-8410
TELEPAX: (415) 39-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                        : 1296 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 69; Conserv
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:|||||||| 123 GEIIWTLQDTQEIKQRV 139

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NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01308
TELECOMMINICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 438 amino acids
amino acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94104
                                                                                                                                US-08-405-496A-23
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48.2%; Score 371.5; DB 1; Length 438;
Best Local Similarity 49.6%; Pred. No. 7.6e-31;
Matches 68; Conservative 28; Mismatches 40; Indels 1.
                                                           APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH N.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDENCES: 32
CORRESPONDENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                             GUUNTRY: UNITED STATES OF AMERICA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-UN-1995
CLASSIFICATION UNMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/985,321
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/429,791
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: A0,027
FILING DATE: 110-DCT-1989
TOTHER APPLICATION NUMBER: A0,027
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIAME E.
RECISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/CATION NUMBER: 40,027
REFERENCE/CATION NUMBER: 40,027
RELEPAX: (415) 39-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
I-BNGTH: 438 amino acids
                                                                                                                                                                                                                                                                                                                                     STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                            ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SI
Sequence 23, Application US/08480604A
Patent No. 5736139
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 438 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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128 NKIIWTLQDTAGNNQKL 144

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68 SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
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48.2%; Score 371.5; DB 1; Length 438;
Best Local Similarity 49.6%; Pred. No. 7.6e-31;
Matches 68; Conservative 28; Mismatches 40; Indels 1
Sequence 23, Application US/08405496A
| Patent No. 5919665
| GENERAL INFORMATION: WILLIAMS, JAMES A.
| TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF INVENTION: WACCINE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF MONTACONE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF MONTACONE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF MONTACONE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF WONTACONE FOR CLOSTRIDIUM BOTULINUM
| TITLE FOR FOR CLOSTRIDIUM FOR CLOSTRIDIUM FOR CLOSTRIDIUM FOR CL
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: US/08/405,496A
FILING DATE: US/08/405,496A
FILING DATE: 125-0CT-1994
PRIOR APPLICATION NUMBER: US/08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATPONIEY/AGENT: NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATPONIEY/AGENT: NUMBER: US 07/429,791
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123 GEIIWTLQDTQEIKQRV 139
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                                                                                                                                                                                                                       APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE 3.
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 48.2%; Score 371.5; DB 2
Best Local Similarity 49.6%; Pred. No. 7.6e-31;
Matches 68; Conservative 28; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
APPLICATION DATA: US 08/161,907
FILING DATE: 02-DEC-1993
FILING DATE: 02-DEC-1993
APPLICATION DATA: US 07/985,321
FILING DATE: 04-DEC-1992
PRICA PAPLICATION DATA: US 07/429,791
FILING DATE: 13-OCT-1999
ATTONNEY, AGENT INPORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 02.837
TELECHONE: (415) 705-8410
                                                                                                                                                  Sequence 23, Application US/09084517
Patent No. 6613329
GENERAL INFORMATION:
128 NKIIWTLQDTAGNNOKL 144
                                        123 GELÍWTLÓDTOEIKÓRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-WAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-09-084-517-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                              RESULT 9
US-09-084-517-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LILYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                       APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PIRCA, JOSEHR R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.2%; Score 371.5; DB 2
Best Local Similarity 49.6%; Pred. No. 7.6e-31;
Matches 68; Conservative 28; Mismatches 40
                                                                                                                                                                                                                                                                                               SSEE: MEDLEN & CARROLL, LLP
1: 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
  US-08-915-136-23
; Sequence 23, Application US/08915136
; Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 705-8410
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amino acid
                                                                                           JOHN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-915-136-23
                                                                                                                                                                                                                                                                                                                                                                         CALIFORNIA
                                                              GENERAL INFORMATION:
APPLICANT: KINK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  94104
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                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                         STREET:
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STATE:
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8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
                                                                         68 SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 462;
                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRIES

ZIP: 94104

ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BAR PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A

TILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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CIASSIFICATION: 474
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 13-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 00,027
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    128 NKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 397-8338
FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.61
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                              US-08-405-496A-26
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INFORMATION F
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                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: STAFFORD,
APPLICANT: STAFFORD,
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND STAFFORD,
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
CITY: SAN FRANCISCO
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CULF: JALCA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 14-APR-1995

PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/405,496
FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1997

PRILING DATE: 31-OCT-1997

APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989

APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989

APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                   Sequence 26, Application US/08480604A
Patent No. 5736139
                   128 NKIIWTLODTAGNNOKL 144
                                                             123 GEIIWTLODIQEIKORV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 68; Conserva
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                                                                                                                                                           US-08-480-604A-26
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68 SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127

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SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
CORRESPONDENCE: 30
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.2%; Score 371.5; DB 2;
49.6%; Pred. No. 8.2e-31;
iive 28; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONIFOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION NUMBER: US 08/161,907
PRIOR APPLICATION NUMBER: US 08/161,907
PILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/92,791
APPLICATION NUMBER: US 07/429,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09084517
Patent No. 6613329
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER 8
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 705-8410
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147 GEIIWTLQDTQEIKQRV 163
                                                                                                                                                                                               128 NKIIWTLODTAGNNOKL 144
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                               RESULT 13
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88 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         ANTITOXIN FOR TREATMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BW PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.2%; Score 371.5; DB 2;
49.6%; Pred. No. 8.2e-31;
iive 28; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PAPLICATION DATA:
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGCLIA, DIANE E.
REGISTRATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: OPPLICATION NUMBER: OPPLO-1763
REFERENCE/DOCKET NUMBER: OPPLO-1763
REPERSENCE/DOCKET NUMBER: OPPLO-1763
                                                                                                                                                                                                                                                                                         APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                           Sequence 26, Application US/08915136
Patent No. 6290960
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                         128 NKIIWTLQDTAGNNQKL 144
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147 GEIIWTLQDTQEIKQRV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                  RESULT 12
US-08-915-136-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
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                                                                                               SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
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LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
                              28 LLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLES 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 2-ANG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 2-DEC-1996
ATTORNEY/AGENT IRFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.1%; Score 355; DB 2;
47.3%; Pred. No. 1.5e-28;
tive 33; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION: 10FORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09255829 Patent No. 6461617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                            128 NKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                        :||||||||||||
147 GEIIWTLQDTQEIKQRV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-255-829-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 69; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
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Sequence 220, Application US/10360101

Patent No. 6861236

GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION Export and modification of (poly) peptide in the lantibiotic way
FILE REFERENCE: 2183-5673

CURRENT APPLICATION NUMBER: US/10/360,101

CURRENT APPLICATION NUMBER: EP 02077066.8

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

SOFTWARE: Patentin version 3.1

SEQ ID NO 220

LENGTH: 1290
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900 LISSANSKIRVIQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NN 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YINDKILLLYFUKLYKKIKDNSILDMRYBNNKFIDISGYGSNISINGDVYIYSTURNOFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.1%; Score 355; DB 2; Length 12 Best Local Similarity 47.3%; Pred. No. 1.7e-28; Matches 69; Conservative 33; Mismatches 38; Indels
960 SGWKISIRGNRIIWTLIDINGKTKSV 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||| : : ||||| | : : SGWKISIRGNRIIWTLIDINGKTKSV 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: March
Job time : 18.7077 secs
                                                                                                         US-10-360-101-220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

Result

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Publication No. US20020081304A1
GENERAL INFORMATION:
APPLICANT: Blmore, Michael J.
APPLICANT: Minton, Nigel P.
APPLICANT: Pasechnik, Vladimir A.
APPLICANT: Titball Richard W.
TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STAIL:
COUNTRY: USA
ZIP: 22201-4741
ZIP: PROBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
...THOM DATA
...ATION DATA
...ANG/981,087A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20020081304Alth Glebe Rd.
                                                                                                                                                                                                                                                                US-09-910-186A-14
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIPICATION 1424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511909.5
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REPRENCE/DOCKET NUMBER: 124-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 144 amino acids
TYPE: amino acid
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                               2, 2006, 01:11:03; Search time 57.2993 Seconds (without alignments) 1050.055 Million cell updates/sec
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                                                                                                                                                                                                                                 1 SYTNDKILILYFNKLYKKIK......LNYNKIIWTLQDTAGNNQKL 144
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| / cgn2 6/ptodata/1/pubbaa/USO7_PUBCOMB.pep:*
2: / cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: / cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
4: / cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
5: / cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
6: / cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-478-516-23
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JS-10-205-516-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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; Sequence 16, Application US/09910186A
; Publication No. US20030009025A1
; GENERAL INFORMATION:
; APPLICANT: OUS. Army Medical Research & Material Command
; TITLE OF INVENTION: NEUROTONIN
; TITLE OF INVENTION: NEUROPONIN
; FILE REFERENCE: A3326.A 06725.0107
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US/09/910,186A
; CURRENT FILING DATE: 2000-05-12
; PRIOR PLICATION NUMBER: 60/133,865
; PRIOR PLICATION NUMBER: 60/133,865
; PRIOR PLICATION NUMBER: 60/133,865
; PRIOR PLICATION NUMBER: 60/133,866
; PRIOR PLICATION NUMBER: 60/133,866
; PRIOR PLICATION NUMBER: 60/133,866
; PRIOR PLICATION NUMBER: 60/133,866
; PRIOR PLICATION NUMBER: 60/133,867
; PRIOR PLICATION NUMBER: 60/133,867
; PRIOR PLICATION NUMBER: 60/133,867
; PRIOR PLICATION NUMBER: 60/133,867
; PRIOR PLICATION NUMBER: 60/133,868
; PRIOR PLICATION NUMBER: 60/133,868
; PRIOR FILING DATE: 1999-05-12
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                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION NUMBER: US/08/981,087A
PRIOR APPLICATION DATE: 22-MAY-1998
FILING DATE: 12-JUN-1996
PILING DATE: 12-JUN-1996
PILING APPLICATION DAMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTAMFORM ATHORN
NAME: CTAMFORM ATHORN
NAME: CTAMFORM ATHORN
NAME: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CTAMFORM ATHORN
NAME: 25-JUN-1995
ATTORNEY/AGENT APPLIANT R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 124-688
TELEPHONE: 109-816-4000
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100.0%; Score 770; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.3e-64;
Matches 144; Conservative 0; Mismatches 0;
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                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                 ZIP: 22201-4741
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                          MEDIUM TYPE:
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APPLICANT: Fark, Jung-Beak
APPLICANT: Park, Jung-Beak
APPLICANT: Maksymowych, Andrew
TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-9601
CURRENT APPLICATION NUMBER: uS/10/452,024
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin version 3.2
SEQ ID NO 173
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                                                                                                                                                                                                                                                                  61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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                                                               Gaps
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   Length 144;
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APPLICANT: Minton, Nigel P.
APPLICANT: Pasechnik, Vladimir A.
APPLICANT: Tital, Richard W.
TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20020081304A1th Glebe Rd. 8th floor
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100.0%; Score 770; DB 2;
100.0%; Pred. No. 1.2e-64;
ive 0; Mismatches 0;
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100.0%; Pred. No. 3.5e-64;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Clostridium botulinum
                                                         Matches 144; Conservative
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Best Local Similarity
Matches 144; Conserva
Query Match
Best Local Similarity
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US-08-981-087A-1
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100.0%; Score 770; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.3e-64;
Matches 144; Conservative 0; Mismatches 0; Indels (
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
FILE REPERENCE: A33626-A 067252.0107
CURRENT APPLICATION NUMBER: US/09/910,186A
CURRENT PILLING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR PILLING DATE: 2000-07-06
PRIOR PELICATION NUMBER: 60/133,865
PRIOR PILLING DATE: 1999-05-12
PRIOR PILLING DATE: 1999-05-12
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PRIOR PILLING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,869
PRIOR PLING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,873
PRIOR FILING DATE: 1999-05-12
PRIOR PLING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FestSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/09910186A Publication No. US20030009025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-910-186A-16
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Length 432;

DB 3;

100.0%; Score 770;

Query Match

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APPLICANT: Park, Jung-Beak
APPLICANT: Makeymowych, Andrew
APPLICANT: Makeymowych, Andrew
APPLICANT: Makeymowych, Andrew
TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REPRENCE: 9855-9611
CURRENT APPLICATION NUMBER: 02/10/452,024
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2002-06-31
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin version 3.2
SEQ ID NO 178
LENGTH: 432
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APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERENCE: 1581.022000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1000-04-07
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Pred. No. 4.3e-64;
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Best Local Similarity 100.0%; Pred. No. 4.3e-64;
Matches 144; Conservative 0; Mismatches 0;
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Publication No. US20040013687A1
GENERAL INFORMATION:
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APPLICANT: Shone, Clifford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Clostridium botulinum US-10-452-024-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 144; Conservative 0
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RESULT 8
US-10-478-516-5
; Sequence 5, Application US/10478516
; Publication No. US20040208889A1
; GENERAL INFORMATION:
; APPLICANT: Suton, John M.
; APPLICANT: Shone, Clifford C.
; TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
; TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
; CURRENT PILION UNMER: US/10/478,516
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR PLICATION NUMBER: PCT/GB02/02384
; PRIOR FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 32
; SOFTHARE: Patentin Version 3.1
; SEQ ID NO 5
; LENGTH: 645
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100.0%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.9e-64;
Matches 144; Conservative 0; Mismatches 0;
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100.0%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.9e-64;
Matches 144; Conservative 0; Mismatches 0;

// OTHER INFORMATION: synthetic construct
US-10-130-973A-8

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SOFTWARE: PatentIn version 3.0
                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial sequence
                                       SEQ ID NO 8
LENGIH: 645
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; Sequence 6, Application US/10478516; Publication No. US20040208889A1

US-10-478-516-6

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; OTHER INFORMATION: thrombin linker, diphtheria toxin translocation domain, BoNT/F-HO
US-10-478-516-6
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US-10-478-516-7
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Publication No. US2004020889A1
GENERAL INFORMATION:
APPLICANT: Sutcon, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REPRENCE: 1581.1000000
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARR: Patentin Version 3.1
SEQ ID NO
                    APPLICANT: Sutton, John M.

APPLICANT: Shore, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.1000000
CURRENY APPLICATION WUMBER: 9210/478,516
CURRENY FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR FILING DATE: 2001-05-24
SOFTWARE: Patentin version 3.1
SSEQ ID NOS: 32
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100.0%; Score 770; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 7e-64;
Matches 144; Conservative 0; Mismatches 0; Indels
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100.0%; Score 770; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 7e-64;
Matches 144; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
BENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              LENGTH: 657
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: CONSTRUCTS for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
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; Pred. No. 9.7e-64;
0; Mismatches 0;
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%; Pred. No. 7.4e-64;
0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: SYNThetic construct US-10-130-973A-4
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                                                                      FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-130-973A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WKISLNYNKIIWTLODTAGNNOKL 144
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PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10130973A Publication No. US20030147895A1 GENERAL INFORMATION:
                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 144; Conservative 0;
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Best Local Similarity 100.
Matches 144; Conservative
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                       TYPE: PRT
ORGANISM: Artificial
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US-10-130-973A-4
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APPLICANT: Sutcon, John
APPLICANT: Sutcon, John
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION UMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                                                                                                                                                                                              APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Sliman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR PILING DATE: 2000-12-04
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
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287 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 346
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PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOGTWARE: Patentin version 3.0
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                                                                                                      WKISLNYNKIIWTLODTAGNNOKL 370
                                                                                                                                                                                                                            Sequence 12, Application US/10130973A Publication No. US20030147895A1
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                 Publication No. US20030147895A1
GENERAL INFORMATION:
APPLICANT: Shone, Clifford
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GENERAL INFORMATION:
APPLICANT: Shone, Clifford
APPLICANT: Structon, John
APPLICANT: Stlman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPRENENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: PCT/GB00/04644
FRIOR APPLICATION NUMBER: PCT/GB00/04644
FRIOR PILING DATE: 2000-12-04
FRIOR FILING DATE: 199-12-02
FRIOR FILING DATE: 199-12-02
FRIOR FILING DATE: 199-12-02
FRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-04-07
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH 887
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Sequence 26, Application US/10478516

Publication No. US20040208889A1

GENERAL INFORMATION:

APPLICANT: Sutton, John M.

APPLICANT: Shone, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.1000000

CURRENT APPLICATION NUMBER: US/10/478,516

FRIOR APPLICATION NUMBER: PCT/GB02/02384

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 1e-63;
Matches 144; Conservative 0; Mismatches
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ORGANISM: Artificial sequence
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Best Local Similarity
Matches 144; Conserva
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LENGTH: 979
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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60

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Db 549 SYTNDKILLYFONKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVIYSTNRNQF 608

Qy 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120

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Qy 121 WKISLNYRKIIWTLQDTAGNNQKL 144

Db 669 WKISLNYRKIIWTLQDTAGNNQKL 692

Search completed: March 2, 2006, 01:17:47
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Maximum Match 100%
Listing first 45 summaries
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## STIMMARIES

	Description	Sequence 5, Appli	Sequence 8, Appli		Sequence 26, Appl	18,	3,	Sequence 6, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 30, Appl	Sequence 22, Appl	Sequence 24, Appl	Sequence 141, App	Sequence 90, Appl	$\sim$		Sequence 131, App	Sequence 18, Appl	Sequence 6, Appli				Sequence 2414, Ap
SUMMARIES	QI	US/11/062	US/11/062	US-10-909-769-28	US-10-909-769-26	US-10-909-769-18	US/11/062	US/11/062	US/11/062	US/11/062	US-11-077-550-20	US-10-909-769-20	US-10-909-769-30	US-10-909-769-22	US-10-909-769-24	US-11-077-550-141	US-11-052-554A-90	US-11-098-686-10240	US-11-052-554A-109	US-11-036-532A-131	US-11-091-643-18	US-11-070-575-6	US-11-087-099-3020	US-11-057-058-66	US-11-091-643-20	US-10-793-626-2414
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26 75 9.7 248 7 US-II-062-554A-70 Sequence 70, Appl 28 74.5 9.7 741 7 US-II-089-551A-46 Sequence 70, Appl 29 74.5 9.7 741 7 US-II-089-551A-46 Sequence 91, Appl 29 74.5 9.7 741 7 US-II-089-551A-46 Sequence 91, Appl 29 74.5 9.7 290.2 7 US-II-087-099-4084 Sequence 10.84, Appl 31 73.5 9.5 874 7 US-II-087-099-10.85 Sequence 10.84, Appl 32 73.5 9.5 874 7 US-II-091-64.4 Sequence 10.83, Appl 34 73 9.5 878 7 US-II-091-64.4 Sequence 10.83, Appl 36 73 9.5 883 7 US-II-091-64.4 Sequence 11.8 Sequence 20.8 Appl 36 73 9.5 883 7 US-II-091-64.4 Sequence 21.8, Appl 37.2 9.5 9.4 42.3 7 US-II-087-099-286 Sequence 21.8, Appl 37.2 9.4 42.3 7 US-II-087-099-286 Sequence 21.8, Appl 40 72.5 9.4 42.4 7 US-II-036-522A-12 Sequence 12.4, Appl 41 72.5 9.4 42.4 7 US-II-036-522A-12 Sequence 12.4, Appl 41 72.5 9.4 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 41 72.5 9.4 42.5 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.7 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Sequence 13.4, Appl 42.4 7 US-II-036-522A-13 Se	•	
9.7 248 7 US-II-052-554A-70 Sequence 9.7 248 7 US-II-089-551A-46 Sequence 9.7 2902 7 US-II-089-551A-46 Sequence 9.6 362 7 US-II-087-099-4084 Sequence 9.6 363 7 US-II-087-099-4084 Sequence 9.6 365 6 US-IO-873-528-164 Sequence 9.5 588 7 US-II-087-099-10263 Sequence 9.5 1316 7 US-II-097-099-10263 Sequence 9.5 465 7 US-II-091-643-4 Sequence 9.5 465 7 US-II-092-54A-215 Sequence 9.5 463 7 US-II-082-554A-215 Sequence 9.5 4081 7 US-II-082-554A-215 Sequence 9.4 423 7 US-II-082-554A-215 Sequence 9.4 423 7 US-II-036-532A-124 Sequence 9.4 423 7 US-II-036-532A-124 Sequence 9.4 425 7 US-II-036-532A-136 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 425 7 US-II-036-532A-138 Sequence 9.4 458 7 US-II-036-532A-130 Sequence	26, Appl 26, Appl 39, Appl 39, Appl 30,	
9.7 248 7 US-11.052-554A-70 9.7 741 7 US-11.082-551A-46 9.6 363 7 US-11.082-554A-91 9.6 465 6 US-11.087-099-4084 9.5 874 7 US-11.087-099-164 9.5 874 7 US-11.087-099-10263 9.5 1316 7 US-11.091-091-083 9.5 474 7 US-11.091-091-083 9.5 483 7 US-11.091-092-54A-115 9.5 494 423 7 US-11.085-52A-126 9.4 423 7 US-11.036-52A-126 9.4 424 7 US-11.036-52A-136 9.4 425 7 US-11.036-52A-136 9.4 425 7 US-11.036-52A-136 9.4 425 7 US-11.036-52A-138 9.4 425 7 US-11.036-52A-138	( VOI VIAMA VIAMA CALLACTER	
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## ALIGNMENTS

RESULT 1 US/11/062 Sequence 5, Bublication GENERAL INR APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: FILE REFER	SULT 1 /11/062 Sequence 5, Application US/11062471A sequence 5, Application US/11062471A sublication No. US2005025503A1 GENERAL INFORMATION: GENERAL INFORMATION: CILITORY: SHOWE, CILITOR Charles APPLICANT: SHOWE, CILITOR BASSAM APPLICANT: SHOWE, SHOWE, CILITORY: Dassam APPLICANT: SILMAN, Nigel TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells FILE REFERENCE: 1581.0800001 CURRENT APPLICATION NUMBER: US/11/062,471A CURRENT FILING DATE: 12999-11-05 FRIOR APPLICATION NUMBER: G9/831,050 FRIOR FILING DATE: 1999-11-05 FRIOR PRILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 11 SEQ ID NOS: 11 SEQ ID NOS: 11 SEQ ID NO SEC ID NOS: 11
LENGTH: 1059 TYPE: PRT ORGANISM: Ar FEATURE: OTHER INFORM	LENGTH: 1059 TYPE: PRT ORGANISM: Artificial Sequence FRATURE: OTHER: NFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker,
Ouery Match Best Local Matches 14	/if/062/fife Query Match Best Local Similarity 100.0%; Pred. No. 3.1e-63; Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
දු පු	1 SYTNDKILLIYFNKLYKKIKDNSILDMRYENDKFIDISGYGSNISINGDVYIYSTNRNQF 60 
که B	61 GIYSSKESEVNIAQNNDIIYNGRYQNFSISFWYRIPKYENKVNIANNEYTIIDCIRNNNSG 120 
9 9	121 WKISLNYNKIIWTLQDTAGNNQKL 144 

RESULT 2 US/11/062

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APPLICANT: Steward-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris
FILE REFERENCE: ALLEGO10-100 (ROIZ003-146)
CURRENT PEPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 18
LENGTH: 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Substitution of Application US/10909769

Publication No. US20060024331A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strandez-Salas, Ester
APPLICANT: Lin, Wei-Jen
APPLICANT: AppliCANT: Lin, Wei-Jen
APPLICANT: AppliCANT: Cands George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist FILE REFERENCE: ALLEGO10-100 (ROIZO03-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT APPLICANION 1005: 34
CURRENT SILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.2%; Score 571.5; DB 6; 71.7%; Pred. No. 4.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Amino acid sequence of HC
                                                                                                                                                                                                                                                    121 WKISLNYNK---IIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                    531 WKISLRTVRDCEIIWTLQDTSGNKENL 557
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Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.2%
Best Local Similarity 71.7%
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                             APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Baseam
APPLICANT: HALLIS, Baseam
APPLICANT: HALLIS, Baseam
APPLICANT: HALLIS, Baseam
APPLICANT: BILMAN, Nigel
TITLE OF INVENTION Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION Delivery of Superoxide Dismutase to Neuronal
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTURNQF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 770; DB 7; 100.0%; Pred. No. 3.2e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  774 WKISLNYNKIIWTLQDTAGNNOKL 797
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Sequence 8, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
                                                                                                               APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity 80.3%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 144; Conservative
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ORGANISM: Artificial Sequence

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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M
US/11/062,471A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 IYSSKRSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUFONG. Clifford Charles
APPLICANT: SUFONG. Clifford Charles
APPLICANT: SUFONG. John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT PILING DATE: 1090-11-05
PRIOR APPLICATION NUMBER: O9/831,050
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
SPRIOR FILING DATE: 1999-11-05
SPRIOR FILING DATE: 1998-11-05
                                            APPLICANT: SILANA, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.080001
CURRENT APPLICATION NHERR: US/11/062,471A
CURRENT APPLICATION NHERR: US/831,050
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
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46.1%; Score 355; DB 7; Length 1070;
Best Local Similarity 47.3%; Pred. No. 4.6e-25;
Matches 69; Conservative 33; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 49.2%; Score 378.5; DB 7; Best Local Similarity 48.3%; Pred. No. 3.2e-27; Matches 69; Conservative 31; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KISLNYNKIIWTLQDTAGNNQKL 144
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ORGANISM: Artificial Sequence
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SUTTON, John Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687 LPNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW 745
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APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PAPLICATION NUMBER: GB 9824282.9
PRIOR PILING DATE: 1998-11-05
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOPTWARE: PATENTIN VET. 2.1
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                                                                                                                         Length 849;
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                                                                                                                            Query Match
Best Local Similarity 48:3%; Pred. No. 2.4e-27;
Matches 69; Conservative 31; Mismatches 42; Indels
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                   ; CTHER INFORMATION: Amino acid sequence of HC US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KISLNYNKIIWTLODTAGNNOKL 144
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KVSLNYGEIIWTLQDTQEIKQRV 768
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APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 20, Application US/10909769

Formander 20, Application US/10909769

Fublication No. US20060024331A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: April CANT: Lin, Wei-Jen
APPLICANT: April CANT: Lin, Wei-Jen
APPLICANT: April COMPOUNDER With Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: TOXIN COMPOUNDER: US/10/909,769
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT PAPLICATION NUMBER: US/10/909,769
CURRENT PAPLICATION NUMBER: 244-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
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45.2%; Score 348; DB 6;
Best Local Similarity 45.6%; Pred. No. 1.7e-24;
Matches 67; Conservative 35; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-20
                         CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-12-77
PRIOR FILING DATE: 1996-12-77
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
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ORGANISM: Artificial Sequence
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Best Local Similarity
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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
US/11/062,471A-7
                                 62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/11062471A

Publication No. US20050255093A1

GENERAL INFORMATION:

APPLICANT: SUTTON, Clifford Charles

APPLICANT: SUTTON, John Mark

APPLICANT: SUTTON, John Mark

APPLICANT: SILMAN, Nigel

TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells

FILE REPRENCE: 1289.1000001

CURRENT APPLICATION NUMBER: US/11/062,471A

PRIOR PILING DATE: 1999-11-05

PRIOR PILING DATE: 1999-11-05

PRIOR PILING DATE: 1999-11-05

PRIOR PILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 11

SOPTWARE: PATENTIN VUMBER: CB 9824282.9

NUMBER OF SEQ ID NOS: 11

SOPTWARE: PATENTIN VET: 2.1
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                                                                                                                               2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
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46.1%; Score 355; DB 7; Length 1095;
Best Local Similarity 47.3%; Pred. No. 4.7e-25;
Matches 69; Conservative 33; Mismatches 38; Indels
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APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Sutton, J. Mark
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Rayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                                                                               119 SGWKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
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Publication No. US20050244435A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Steward, Lance E. APPLICANT: Lin, Wei-Jen R. APPLICANT: Lin, Wei-Jen Reger APPLICANT: APPLICANT: APPLICANT: Lin, Wei-Jen Roger APPLICANT: ALEGORIA GEORGE TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist CURRENT FILING DATE: 2004-08-02 CURRENT FILING DATE: 2004-08-02 SOFTWARE: Patentin version 3.3 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
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32.5%; Score 250; DB 6; Length 842; 37.7%; Pred. No. 1.6e-15; ive 30; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.4%; Score 249.5; DB 6; Best Local Similarity 36.4%; Pred. No. 1.7e-15; Matches 52; Conservative 32; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1591.0130004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Amino acid segence of HC US-10-909-769-24
                                                                                                                                                                                                                                                              119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                        517 SGWSIGIISNFLVFTLKQNEDSEQSI 542
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Publication No. US20050244435A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shone, Clifford Charles APPLICANT: Quinn, Conrad Padraig APPLICANT: Foster, Keith Alan APPLICANT: Chaddock, John APPLICANT: Marks, Philip APPLICANT: Stancombe, Patrick APPLICANT: Stancombe, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fernandez-Salas, Ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                 55; Conservative
                        Best Local Similarity
Matches 55; Conserv
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        Query Match
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Acki, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REPERENCE: ALLEGO10-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
                                                                                                                                                                                                                                                                                                        APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
APPLICANT: Acki, Kei Roger
TTLICANT: Sachs, George
TTLIE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLEGOIO-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PALENTIN NOS: 34
SOFTWARE: PALENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 LANSENSNITAHQSKEVUYDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTISCIK-ND 524
        509 KLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHNEYTIINCMK-N 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 YTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.4%; Score 319; DB 6;
41.8%; Pred. No. 7.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                           NSGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                  | | | | : | : | : | | | | | | : : : SGWKVSIKGNRIIWTLIDVNAKSKSI 550
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                                                                                                                                                                                                                          Sequence 30, Application US/10909769 Publication No. US20060024331A1 GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 842
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LENGTH: 855
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Best Local S
Matches 61
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Search completed: March 2, 2006, 01:18:29 Job time : 6:84687 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein March 2, 2006, 00:31:42; Search time 68.993 Seconds (without alignments) 917.057 Million cell updates/sec Run on:

Title: Perfect score:

US-08-981-087B-3 761 1 VFNYTQMISISDYINKWIFV......ITQNSNFLNINQQRGVYQKP 144 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

geneseqp2003as:\*geneseqp2003bs:\* geneseqp1980s:\* депевефр1990в: geneseqp2002s: geneseqp2001s: A\_Geneseq\_21:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:

geneseqp2004s:

#### SUMMARIES

	Description	Aaw09016 Immunogen			_	_	_				Aae07893 Modified	Aae07890 Modified	_	_	Aae07901 C. botuli	Aay93309 A mangane	Aay93312 A mangane	_		_	_	Aab04095 Botulism	Aay77137 Synthetic	_	Aaw68396 Clostridi
071111100	ID	AAW09016	AAW09014	AAY77138	AAB04103	AAB04096	AAE07894	AAE35692	AAE35693	AAE35694	AAE07893	AAE07890	AAE07892	AAE35713	AAE07901	AAY93309	AAY93312	AAE07900	AAE35711	AAE35710	AAW68399	AAB04095	AAY77137	AAB04094	AAW68396
	DB	7	7	m	4	4	4	9	9	9	4	4	4	9	4	m	e	4	9	9	7	4	m	4	N
٠	Length	144	431	432	432	432	645	645	657	657	685	862	887	979	1032	1059	1084	1092	1192	1192	448	419	449	449	452
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	80.4	65.4	65.4	65.4	65.4
	Score	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	612	497.5	497.5	497.5	497.5
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Aaw68395 Clostridi Aae07898 Modified Aab36303 BonT/A pr Adw24418 C botulin	ш ш д ш	Aab04090 Botulism Aab04088 Botulism Aar95008 Type A ne	Adwessey Closting Aay77134 Synthetic Aaw68391 Clostridi Aar95009 Type A ne Aaw68390 Clostridi	
AAW68395 AAE07898 AAB36303 ADW24418	ADZ60271 ADZ60276 AAY77142 AAB04089	AAB04090 AAB04088 AAR95008	AAW68389 AAY77134 AAW68391 AAR95009	AAY77140 ADZ69764 AAY93307 AAY93310 AAU99339
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451 660 382 382	382 425 432 432	437 437 438	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	837 837 1067 1092 1295
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495.5 466 440.5	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	440.5 440.5 5.05	4440.5 4440.5 4440.5	4440.5 4440.5 4440.5 440.5 640.5
25 27 27	3000		9 7 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 0 4 6 6 4 6

### ALIGNMENTS

RESULT 1

Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism. Immunogenic type F botulinum toxin polypeptide (aa992-1135). Clostridium botulinum; type F strain Langeland AAW09016 standard; protein; 144 AA (first entry) (revised) WO9641881-A1 17-OCT-2003 31-MAR-1997 AAW09016; AAW09016

27-DEC-1996.

96WO-GB001409. 12-JUN-1996; (MICR-) MICROBIOLOGICAL RES AUTHORITY

95GB-00011909.

12-JUN-1995;

Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA;

WPI; 1997-065467/06.

Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.

Claim 5; Page 18-19; 37pp; English.

Novel polypeptides (AAM09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BoNT/F). They lack the Lothain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine proden. Recombinant polypeptides can be produced in transformed host cells, as fusion proteins, e.g. with malcose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 144 AA;

Query Match

100.0%; Score 761; DB 2; Length 144;

VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120

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us-08-981-087b-3.rag

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                                                                                                                                    VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                              VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a type F botulinum neurotoxin (BONT/F), and can neguced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with maltose bhinding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                     VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                               1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sotulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism.
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                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic type F botulinum toxin heavy chain (aa848-1278).
                 0; Indels
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   Pred. No. 6.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum; type F strain Langeland
                 0; Mismatches
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                                                                                                                                                                               TDKSITQNSNFLNINQQRGVYQKP 144
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                                                                                                                                                                                                            121 TDKSITQNSNFLNINQQRGVYQKP 144
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                                                                                                                                                                                                                                                                                             AAW09014 standard; protein; 431 AA
100.0%;
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(first entry)
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                 Matches 144; Conservative
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 Best Local Similarity
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31-MAR-1997
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The invention relates to novel vaccines that induce a protective immune response against botulinum neurotoxin (BoNT) serotypes A, B, C, D, E, F and G (BoNTA-BonTG). The vaccine of the invention is novel recombinant comprising a vector, and at least one nucleic acid fragment comprising a vector, and at least one nucleic acid fragment comprising a vector, and at least one nucleic acid fragment comprising a C-terminal heavy chain fragment (Hc) from BoNT serotypes A-CG in preferred embodiments of the invention, the vector is a Venezuelan equine encephalitis virus (VEE) replicon vector. Use of this vector results in the production of large amounts of a protein encoded by a sequence cloned into the replicon. The constructs are used to produce vaccines against botulism. The proteins can also be used as diagnostic tools for the diagnosis of botulism. The transformed host cells can be used to analyse the effectiveness of drugs and agents which inhibit toxin effects. The vaccine currently used against botulism is dangerous and expensive to produce, and contains formalin, which is very painful for the recipient. Also, the vaccine is incomplete, in that only 5 of the 7 serotypes are represented in the formulation. The novel vaccine of overcomes these problems, as it is easily purified, and available in large quantities. It is also expressed in the lymph nodes for a better immune response. Sequences AAY77134-Y77139 represent synthetic BoNT Hc fragments used in the present invention. The DNA encoding these sequences had been optimised for codon usage for expression in yeast. Note: This sequence is not given in the specification, but is decoded from the BONTF CC Hc DNA sequence given on pages 45-46
205 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Botulinum neurotoxin; heavy chain; BoNT; serotype F; C-terminal fragment; Venezuelan equine encephalitis virus replicon; VBE; botulism; vaccine; diagnosis; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Botulinum neurotoxin vaccine comprising a fragment from botulinum toxin serotypes A-G, is used for inducing an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic botulinum neurotoxin serotype F (BoNTF) C-terminal fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith JF, Parker M, Dertzbaugh MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                  TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                             AAY77138 standard; protein; 432 AA.
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99US-0133870P
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N-PSDB; AAZ87216.
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145 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI

1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDBKSISNLGDIHVSDNILFKI

Best Local Similarity 100. Matches 144; Conservative

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Gaps

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Indels

Length 432;

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Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a dichain early chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT)
to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                                                                                   206 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDFSILKDFWGNYLLYNKRYYLLNLLR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                                                                                                                                    146 VPNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                             VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                                                                                                                                                  1 VENYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulism toxin heavy chain C-terminal sequence (serotype F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lapenotiere H;
                                                                                                                                  / Match 100.0%; Score 761; DB 4; Local Similarity 100.0%; Pred. No. 2.6e-73; hes 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
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                                                                                                                                                                                                                                                                                                                                                                               TDKSITONSNFLNINOORGVYOKP 144
                                                                                                                                                                                                                                                                                                                                                                                                         AAB04096 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 9b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0133865P.
99US-0133866P.
99US-0133867P.
99US-0133868P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith LA, Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-016048/02.
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                                                                                                     Sequence 432 AA;
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12-MAY-1999
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                            205
                                                                                                                                                                                                              61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLALLK 120
                                                                                                                                VENYTOMISISDYINKWIFVTITWNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                       Gaps
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                            Length 432;
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                                                                     0; Indels
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                              Score 761; DB 3;
Pred. No. 2.6e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                           TDKSITQNSNFLNINQQRGVYQKP 289
                                                                                                                                                                                                                                                                     121 TDKSITONSNFLNINQORGVYOKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 18b, 73pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                             AAB04103 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0133865P.
99US-0133866P.
99US-0133867P.
99US-0133868P.
                            Query Match
Best Local Similarity 100.0%;
Matches 144; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium botulinum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA54499.
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29-JUL-1999;
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12-MAY-1999;
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12-MAY-1999;
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Synthetic

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AAB04103 ID AABC

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transformed cells to produce peptide antigens useful for eliciting an timune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as
                                                                                                                                                                                                                                                                                                                                                                 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLMLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                               146 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 205
                                                                                                                                                                                                                                                                                                                                                                                                 206 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 265
                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                               1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDBKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                            Length 432;
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                                                                                                                                                                                                                            100.0%; Score 761; DB 4;
100.0%; Pred. No. 2.6e-73;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDKSITQNSNFLNINQQRGVYQKP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE07894 standard; protein; 645 AA.
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07-APR-2000; 2000GB-00008658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514643/56.
                                                                                                                                                                                              Sequence 432 AA;
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01-NOV-2001
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Hc) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for their preparative substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fushing the binding domain of boculinum neurotoxin type F (BONT)F) with translocation domain of diphtheria neurotoxin. (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
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100.0%; Pred. No. 4.3e-73;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-2002; 2002WO-GB002384.
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Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 645 AA;
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17-JUN-2003
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Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Shone CC;

Sutton JM,

WPI; 2003-167247/16.

Example 12; Page 60-63; 130pp; English

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular intracellular intracellular intracellular interacellular interion.
                               Example 12; Page 57-60; 130pp; English.
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Sequence 645 AA;

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418
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                                                               1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                    419 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                      359 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                    Gaps
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100.0%; Score 761; DB 6; Length 645; 100.0%; Pred. No. 4.3e-73; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                          Matches 144; Conservative
   Query Match
Best Local Similarity
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AAE35693 standard; protein; 657 AA
            (first entry)
            17-JUN-2003
       AAE35693;
AAE35693
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BoNT/F-Hc-DipT HN domain-thrombin linker fusion construct.

infection, Prion disease, Alzheimer' disease, hypersecretion disorder, muscle spaem, COPP, bronchitis, chronic obstructive pulmonary disease, torticolis, blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F, translocation domain; HN domain; DipT, Hc; binding domain; Apoptosis; therapy; inflammatory mediator; intracellular trafficking botulinum type F neurotoxin

Corynebacterium diphtheriae Clostridium botulinum. Unidentified. Chimeric

WO200296467-A2

05-DEC-2002

21-MAY-2002; 2002WO-GB002384

24-MAY-2001; 2001GB-00012687

Corynebacterium diphtheriae. Clostridium botulinum. Unidentified.

Chimeric

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular inflection and regulating nitric oxide release from cells! The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular crafticking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for crafticking, for modulating expression of cell-surface markers and for inhibiting muscle spaems such as blephorospsam, toricols and construct comprising Orthodorers uch as chronic obstructive pulmonary disease comprising Orthodorer such as chronic obstructive pulmonary disease comprising Correcterium disphtheriae diphtheriat toxin translocation domain (bip7-HN domain), botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BoNT/F-Hc-DipT HN domain-factor Xa linker fusion construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE35694 standard; protein; 657 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     botulinum type F neurotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 657 AA;
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Best Local
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superoxide dismutase; SOD; botulinum neurotoxin type F; BoNT/F.
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Matches 144; Conservative
                                                                           Clostridium botulinum
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                                                          Influenza virus
                                                                                                                                                          WO200158936-A2.
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                                                                                                                     Chimeric
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AC AAE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain, botulinum type F neurotoxin binding domain (BoMT/F-HG) from Clostridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                        Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing and reversing danger to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as Diephorospasm, torticolis and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construc
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for treatment selected from promoting or inhibiting survival of cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 761; DB 6; Length 657; 100.0%; Pred. No. 4.4e-73; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                           Example 12; Page 63-65; 130pp; English.
                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY
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                                                                                                                                   24-MAY-2001; 2001GB-00012687
                                                                                         21-MAY-2002; 2002WO-GB002384
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Matches 144; Conserv
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            WO200296467-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (active y terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell, which comprises the therapeutic cells that binds to the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are cells. The polypeptide constructs are useful for the invention are cells. The polypeptide constructs are useful to treat disorders of the CS including neuronal cells. They are useful to treat disorders of the CS including neurodespenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain supercoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MSDO), from CS and inuspection the class of the conjugate comprises bacterial Mn-superoxide dismutase (MSDO), from CS it main to be cleaved by factor Xa, chain and a neuronal cell-specific conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDFSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding domain from botulinum neurotoxin type F (BoNT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE07890 standard; protein; 862 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDKSITQNSNFLNINQQRGVYQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 43; 50pp; English.
Geobacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2000; 2000WO-GB004644.
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07-APR-2000; 2000GB-00008658
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carbox terminal half of heavy chain (HC) of a neuroctoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic domain of a clostridial toxin. Polypeptides of the invention are a HN domain of a clostridial toxin. Polypeptides of the invention are caful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase (MnSOD), from conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from than substocation domain from diphtheria neurotoxin and a neuronal cell-correction denain from botulinum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 635
                                                                        Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                      Modified clostridial heavy chain-superoxide dismutase conjugate #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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Best Local Similarity 100.0%; Score 761; DB 4; Length 862;
Best Local Similarity 100.0%; Pred. No. 6.2e-73;
Matches 144; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 40; 50pp; English.
                                                                                                                                                                              Geobacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2000; 2000WO-GB004644
                                                                                                                                                                                              Corynebacterium diphtheriae.
Clostridium botulinum.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 862 AA;
                                                                                                                                                                                                                                                                                                      WO200158936-A2.
01-NOV-2001
                                                                                                                                                                                                                                                                                                                                               16-AUG-2001
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                                                                                                                                                                                                                                                                  Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shone
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carbox therapeutic agent to a neuronal cell, which comprises a binding domain carbox (carbox) terminal half of heady chain (HC) of a neurotoxin, designated as terminal half of HC, designated as HN), that translocation domain is not a terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful to treat disorders of the substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase (Chispeptide (MNSOD), MNSOD from Bacillus steacothermophilus, conjugate comprises a mitochondrial leader sequence from human Mn-conjugate comprises a mitochondrial leader sequence from human from the treatment of diphtherial neurotoxin and a neuronal cell-specific binding domain from conjugate continum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                 Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                             Modified clostridial heavy chain-superoxide dismutase conjugate #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.0%; Pred. No. 6.4e-73;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                   AAE07892 standard; protein; 887 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Page 42; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silman N;
                                                                                                                                                                                                                                                                                                                                      Geobacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000; 2000WO-GB004644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99GB-00028530
                                                                                                                                                                                                                                                                                                                                                          Corynebacterium diphtheriae.
Clostridium botulinum.
Synthetic.
                                                                                                                       01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shone CC, Sutton JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2001.
                                                                                AAE07892;
                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric
RESULT 12
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601-VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 660

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TDKSITONSNFLNINOORGVYOKP

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Thu Mar

the exemplification of the invention

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target call. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, relasse of an inflammatory mediator from cells, division of cells and treating intracellular call in the manufacture of a medicament for treating an eneronal cell, for intracellular infection, for interfering with intracellular call, for intracellular call, for intracellular call in the manufacture of a medicament for treating an eneronal cell, for intracellular infection, for interfering with intracellular call into modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer disease and wide range of disorders including muscle spasms such as blophorospasm, torticolis and characterium disputheriae observed to observe comprising corpusatorer such as chronic observed; a fusion construct comprising Corynebacters much as chronic observed; a fusion construct comprising Corynebacterium dipptheriae diphtheriae toxin translocation comprising homein (DipT-HN domain), botulinum and factor Xa linker peptide and Yersinia pestis targetted effector protien YopT. This sequence is used in
                              Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                            BONT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm, CODD, bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain, Dipf; HC; binding domain; botulinum type F neurotoxin; targetted effector protien; Yopf.
VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 12; Page 110-114; 130pp; English
                                                                                                                      TDKSITQNSNFLNINQQRGVYQKP 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                 AAE35713 standard; protein; 979 AA
                                                                                        121 TDKSITQNSNFLNINQQRGVYQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2001; 2001GB-00012687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shone CC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis.
Unidentified.
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                                              661
                                                                                                                                                                                                                                                                                             AAE35713;
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial coll, where the translocation domain is not a HN comain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for delivering therapeutic colls. They are useful in gene therapy. The present sequence and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum neurodestic neurotoxin translocation domain with botulinum can neuronal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                             812
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                                                                                                                                                                                                                                                                           752
                                                                                                                                                                                                                                                                                                                                          VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                    753 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                                                                                                                                    1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                              693 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                            Gaps

    botulinum C2 translocation domain with BoNT/F-binding domain #2.

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                                                                         Length 979;
                                                                  Score 761; DB 6;
Pred. No. 7.3e-73;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE07901 standard; protein; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDKSITQNSNFLNINQQRGVYQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDKSITONSNFLNINGORGVYOKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silman N;
                                                                      100.08;
                                                                                                  100.0%;
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07-APR-2000; 2000GB-00008658.
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                                                                                                                                         Conservative
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                                                                                                  Similarity
Sequence 979 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200158936-A2
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                                                                                                                                                              746 VPNYTQMISISDYINKWIPVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 805
                                                                                                                                                                                                             VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                  Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                                                                                                       9
                                                                                                                                       1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manganese superoxide dismutase, Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease;
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                                                                Length 1032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A manganese superoxide dismutase (Mn-SOD) construct
                                                                Query Match
100.0%; Score 761; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 144; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                               TDKSITQNSNFLNINQQRGVYQKP 889
                                                                                                                                                                                                                                                                                      TDKSITONSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93309 standard; protein; 1059 AA
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Clostridium botulinum.
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                                   Sequence 1032 AA;
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the invention
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                                                                                              1 VFNYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                         61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                    0; Gaps
                                      Length 1059;
                                                                    Indels
                                      Query Match
100.0%; Score 761; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.1e-73;
Matches 144; Conservative 0; Mismatches 0;
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Best Local Similarity
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Job time

Search

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# GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

- protein search, using sw model OM protein

March 2, 2006, 00:39:17; Search time 12.0278 Seconds (without alignments) 1151.928 Million cell updates/sec Run on:

US-08-981-087B-3 761 1 VFNYTQMISISDYINKWIFV......ITQNSNFLNINQQRGVYQKP 144 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	botulinum neurotox	neurotoxin type F	botulinum neurotox	botulinum neurotox	bontoxilysin (EC 3	botulinum neurotox	neurotoxin - Clost	١١	bontoxilysin (EC 3	botulinum neurotox	tentoxilysin (EC 3	botulinum neurotox	botulinum neurotox	botulinum neurotox	progenitor toxin n	botulinum toxin no	nontoxic-nonhemagg	botulinum neurotox	toxin, nontoxic co	botulinum neurotox	botulinum neurotox	flagellar motor sw	ORF MSV140 hypothe	endo-1,4-beta-gluc	tic	toxin B - Clostrid		cytotoxin L - Clos	probable esterase
αI	833411	140813	S21178	· JH0256	BTCLAB	I40645	839791	140631	A48940	S11455	BICLIN	A49777	S46431	S70582	A47708	140817	JC4901	S68218	JQ1467	S46430	I40644	H84938	T28301	140799	AG2560	S10317	870172	I40884	B97148
th DB	28 2	74 2		251 2		296 2		31 2	31 1			31 2	31 2	35 2	52 2	52 2	193 2	193 2	96 2	196 2	165 2	315 2	08 2	460 2	87 2	66 2	67 2	64 2	35 2
Length	1268	1274	1252	125	12	129	120	1291	129	15	13	1291	12	128	1162	1162	11	11	11	11	11	m	Ō	4	1487	23	2367	23	H
% Query Match	81.7	80.4	65.4	65.1	57.9	55.7	39.0	38.9	37.4	32.3	31.6	31.4	31.4	29.6	16.7	15.8	15.4	15.2	15.0	15.0	13.8	12.2	12.1	11.8	11.8	11.7	11.7	11.3	11.2
Score	622	612	497.5		440.5	423.5		296	284.5	245.5	240.5	239	239	225	127	120	117	116	114	114	105	92.5	92	89.5	89.5	89	89	98	82
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hypothetical prote DNA-directed RNA p	hypothetical prote hypothetical prote	hypothetical prote probable membrane	regulatory protein protein 0377 - mal	hypothetical prote	carbamoyl-phosphat	hypothetical prote	26S proteasome reg	multiple banded an	hypothetical profe	rep protein - slim
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30	3 3 3 3	3 3 4 5	36	38	39	40	42	, 43	44	45

#### ALIGNMENTS

RESULT 1 S33411
botulinum neurotoxin type F - Clostridium Darati C:Soecies: Clostridium barati
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33411; S31860
R; Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Kichardson, P.I.
FEMS Microbiol. Lett. 108, 1.75-182, 1993
A; Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin
A; Reference number: S33411; MUID: 93252228; PMID: 8486245
A;Accesion: S33411
A;Status: preliminary
A; Molecule type: DNA
A;Residues: 1-1268 <tho></tho>
A;Cross-references: UNIPROT:Q45851; UNIPARC:UPI00000BAF8C; EMBL:X68262; NID:G49138; PIDN
C;Superfamily: tetanus toxin

C; Keywords: neurotoxin

ö Gaps ; 0 Query Match

81.7%; Score 622; DB 2; Length 1268;
Best Local Similarity 79.0%; Pred. No. 3.3e-48;
Matches 113; Conservative 16; Mismatches 14; Indels

09 1 VENYTOMISISDYINKWIEVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 셤 8

1043 VGCNDTRYVGIRYFKIFNMELDKTEIETLYHSEPDSTILKDFWGNYLLYNKKYYLLNLLK 1102 61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120 ò 셤

121 TDKSITQNSNFLNINQQRGVYQK 143 ઠ 셤

neurotoxin type F - Clostridium botulinum C;Species: Clostridium botulinum C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004 C;Accession: I40813; S48108

R. EBBE, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.F. FEMS Microbiol. Lett. 96, 225-230, 1992.
A.Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A.Reference number: 140644

A,Accession: 140813 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-1274 <RES> A,Cross-references: UNIPROT:P30996; UNIPARC:UPI0000126B8A; GB:M92906; NID:g144866; PIDN R,Campbell, K.D.; Collins, M.D.; East, A.K. J. Clin. Microbiol. 31, 2255-2262, 1993

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A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48108
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 634-1002 <CAM>
                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP1000016EA7B; EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PI
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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botulinum neurotoxin type E precursor - Clostridium botulinum
C;Species Clostridium botulinum betulinum botulinum
C;Species Clostridium botulinum revision 30-Sep-1993 #text change 31-Dec-2004
C;Accession: S21178; S48107; ŪH0257; B35294; A60027; S18111
E;Whelan, S.M.; Elmocre, M.J.; Bodeworth, N.J.; Atkinson, T.; Minton, N.P.
Bur. J. Biochem. 204, 657-667; 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E:
A;Reference number: S21178; MUID:92174922; PMID:1541280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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; Pred. No. 2.6e-47;
10; Mismatches 14;
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Experimental source: strain Beluga
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82.9%;
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R,Gimenez, J.A.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 82.99
Matches 116; Conservative
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A; Molecule type: protein
A; Residues: 420-427 cGIN-
A; Cross-references: UNIPARC: UPI0000176710
A; Experimental source: strain Beluga
A; Note: this fragment was generated by proteolysis with Lyg-C rather than with trypsin
C; Comment: The Clostridial neurotoxins are highly potent protein toxins that inhibit neu
C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
C; Keywords: neurotoxin
F; H-422, Product: botulinum neurotoxin type E light chain #status predicted <LCH>
F; 412-426/Disulfide bonds: #status predicted
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A;Status: nucleic acid sequence not shown
A;Aclecule type: DNA
A;Residues: 1-27, E',29-1251 <POU>
A;Residues: 1-27, E',29-1251 <POU>
A;Residues: 1-27, E',29-1251 <POU>
A;Cross=references: UNIPARC:INDS095; UNIPARC:UPI000017670D; EMBL:X62088; NID:g40379
A;Cross=references: UNIPARC:13181 and ArCC 43755
B;Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N
A;Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N
A;Tit.le: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E tox:
A;Reference number: S16145; MUID:91237316; PMID:2033376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPARC.UP1000016EA8F; EMBL:X53180; NID:g40407; PIDN:CAA37321.1; PI A,Experimental source: strain BL6340
A.Experimental source: strain BL6340
C.Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release
C.Comment: The heavy chain mediates the binding of toxin to cell receptors while the lid
C.Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem. Biophys. Res. Commun. 183, 107-113, 1992
A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type
A;Reference number: JH0256; MUID:92181428; PMID:1543481
A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the A;Reference number: A60027; MUID:90344918; PMID:2116911
A;Accession: A60027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;2-422/Product: botulinum neurotoxin type E light chain #status predicted <LIG>F;423-1251/Product: botulinum neurotoxin type E heavy chain #status predicted <HEA>F;412-426/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               botulinum neurotoxin type E precursor - Clostridium butyricum
C;Species: Clostridium butyricum
C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change
C;Accession: JH0256; S16145
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llarity 67.4%; Pred. No. 9.3e-37;
Conservative 23; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
65.4%; Score 497.5; DB 2
Best Local Similarity 68.1%; Pred. No. 6.1e-37;
Matches 94; Conservative 21; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : | : | : | NNFIDRRKDSTLSINNIR 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 DKSI-TQNSNFLNINQQR 138
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A,Molecule type: DNA
A,Residues: 1-229,'M',231-252 <FUJ>
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C;Superfamily: tetanus toxin
C;Keywords: disulfide bond: hydrolase; metalloproteinase; neurotoxin; transmembrane prot
F;2-444/Product: bontoxilysin A light chain #status experimental <LGHT>
F;445-1296/Product: bontoxilysin A heavy chain #status experimental <HVY>
F;223,227/Binding site: zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1296 <RES>
A;Ross-references: UNIPROT:Q45894; UNIPARC:UPI000016EA88; EMBL:X73423; NID:g507070; PID
C;Superfamily: tetamus toxin
C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                       Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate
                                                                                                                                                                                                                                                                                                                        Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                                                                                                                                                      E.; Suedhof, T.C.; Jahn, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 DGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSNSGILKDFWGNYLQYDKPYYMLNLF 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum neurotoxin type A - Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40645
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of the light chain of botulinum neurotoxin type
                                                                                                                                    Cross-references: UNIPARC:UPI0000173659
(Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, E. Biol. Chem. 269, 1617-1620, 1994
(Jriche: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins., Reference number: A49708; MUID:94124495; PMID:8294407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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A;Title: Sequence of the gene coding for the neurotoxin (A;Reference number: I40645; MUID:94143603; PMID:8310180
A;Accession: I40645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.7%; Score 423.5; DB 2; 56.9%; Pred. No. 3.2e-30; ive 23; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.9%; Score 440.5; DB 1;
57.6%; Pred. No. 9.3e-32;
tive 26; Mismatches 30;
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   : Partial sequence or suce number: A27000
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                                                                                                                                                                                                                                                                                            Contents: annotation
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                                                          Accession: A27000
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A; Residues: 1-1296 <BIN>
A; Creations: 1-1296 <BIN>
A; Creations: UNIPROT: P10845; UNIPARC: UPI000001386; GB: M30196; NID: 9144864; PIDN:
A; Experimental source: strain 62A, subtype A
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
Biochem. 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin
A; Reference number: S09492; MUID: 90235864; PMID: 2185020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Betley, M.J.; Somers, E.; DasGupta, B.R. ochem. Biophys. Res. Commun. 162, 1388-1395, 1989
Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term Reference number: A33401; MUID:89350959; PMID:2669749
                                                                                                                                                                                                                                                                                                                                                   Dontoxilysin (EC 3.4.24.69) A precursor - Clostridium botulinum
N;Alternate names: botulinum neurotoxin type A
C;Species: Clostridium, botulinum
C;Saccession: A35294; Bequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T.; Kurazono, H.; Wille, M.; Prevert, J.; Wernars, K.; Niemann, H.
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other
A;Reference number: A35294; MUID:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1; Q',3-26,'V',28-1296 <THO>
A;Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
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1885 Lett. 376, 41-44, 1995
A.Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A.Reference number: S67988; MUID:96096783; PMID:8521962
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imenez, J.A.; DasGupta, B.R.
Protein Chem. 12, 351-363, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42,
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                                                                   GCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Botulinum type A neurotoxin digested with pepsin yields 132, Reference number: A53884; MUID:94000342; PMID:8397793
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Residues: 867-880;1148-1217,'Y',1219 <GIM>
Cross-references: UNIPARC:UP100000BBB24; UNIPARC:UP10000173656
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Cross-references: UNIPARC:UP10000173657; UNIPARC:UP10000173658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.; Niece, R.
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NNFINRRTDSTLSINNIR 1112
                                                                                                                                                       DKSITQNS-NFLNINQQR 138
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Iochemistry 26, 4162, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
Molecule type: DNA
Residues: 1-12 <FUJ>
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Residues: 1-35 <BET>
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574
C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574
A;Whalan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. 58, 2345-2354, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the type
A;Reference number: A48940; MUID:92384550; PMID:1514783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: type B, Danish
A,Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this publics
R, Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A,Title: Gene probes for identification of the botulinal neurotoxin gene and specific io
A,Reference number: S48103; MUID:94013372; PMID:8408542
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A;Note: sequence extracted from NCBI backbone (NCBIP:109365)
R;DasGupta, B.R.; Datta, A.
Biochimie 70, 811-817, 1988
A;Title: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A;Reference number: S07155; MUID:89000987; PMID:3139097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the light chains of tetanus to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MOlecule type: DNA
A;Residues: 1-1291 <WHE>
A;Cross-references: UNIPROT:P10844; UNIPARC:UP1000016EA76; GB:M81186; NID:g144734; PIDN
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A,Realdues: 36-217, G',219-224,'S',226-246 <8ZA>
A,Realdues: 36-217, G',219-224,'S', EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PJ
A,Cross-references: UNIPARC:UPI000016EA79; EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PJ
R,Kurazono, H.; Mochida, S.; Binz, T.; Eisel, U.; Quanz, M.; Grebenstein, O.; Wernars,
D, Balol Chem. 267, 14721.14729, 1992
A,Title: Minimal essential domains specifying toxicity of the light chains of tetanus the A,Reference number: A42871; MUID:92340509; PMID:1634516
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A;Readdues: 634-994 «CAM»
A;Readdues: 634-994 «CAM»
A;Readdues: 634-994 «CAM»
A;Readdues: 634-994 «CAM»
A;Experimental source: proteolytic type B, strain NCTC 7273
B;Szabo, B.A.; Pemberton, J.M.; Desmarchelier, P.M.
R;Szabo, B.A.; Pemberton, J.M.; Desmarchelier, P.M.
A;Description: Partial amino acid sequence of botulinum neurotoxin type B and comparis
A;Reference number: $21575
                                                                                                                                                                                                                                                                                                              2 FNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV
                                                                                                                                                                                                                                                                                                                                                                                                                               GCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNL--
                                                                                     Length 1291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Clostridium botulinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LRTDKSI------TQNSNFLNINQQRGVY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bontoxilysin (EC 3.4.24.69) B precursor - Clostridium bo
N;Alternate names: botulinum neurotoxin type B (BoNT/B)
C;Species: Clostridium botulinum
                                                                                 38.9%; Score 296; DB 2; llarity 39.9%; Pred. No. 1.1e-18; Conservative 29; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPARC: UPI00000B3742
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F;231/Active site: Glu #status predicted
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A;Residues: 2-29,'M',31-45 <DAS>
                                                                                                                          Local Similarity
Les 63; Conserv
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Matches
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                                                                                                                 neurotoxin - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: O7-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: 839791
R;Campbell, K; Collins, M.D.; Bast, A.K.
Biochim: Biochys: Acta 1216, 487-491, 1993
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium a A;Reference number: S39791; MUID:94092745; PMID:8268233
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium a A;Reference number: S39791; MUID:94092745; PMID:8268233
A;Accession: S39791
A;Accession: S3797
A;Accession: S3797
A;Accession: S3797
A;Accession: S3797
A;Costatus: T-1297
A;Costatus: T-1297
C;Auperfamily: tetanus toxin
C;Keywords: neurotoxin
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Matches 58; Conservative
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A;Molecule type: protein A;Residues: 442-463, R',465-467 <DA2> A;Cross-references: UNIPARC:UP10000173650 R;Schmidt, J-J; Sathyamoorthy, V; DasGupta, B.R. Arch. Biochem. Biophys. 238, 544-548, 1985

Cross-references: UNIPARC:UPI0000173650

olecule type: protein esidues: 2-17 <SCH2> ross-references: UNIPARC:UPI0000173652

atus: preliminary

atus: preliminary

Gene: pont/p

Accession: S08574

ross-references: UNIPARC:UPI000173652

Molecule type: protein Residues: 2-16 <SCH1>

catus; preliminary

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tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
NiAlternate names: tetanus neurotoxin
CiSpecies: Clostridium tetani
CiSpecies: Clostridium tetani
CiAnte: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Jul-2004
CiAccession: A25689; A25757; A25184; B22194; A60759; S69348; S09364
CiAccession: A25689; A275757; A25184; B22194; A60759; S69348; S09364
RiEisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M.
RiEuso J. 5, 2495-2502, 1986
A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botu
A;Reference number: A25689; MUID:87053814; PMID:3536478
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Little: The complete nucleotide sequence of tetanus toxin.
Fittle: The complete nucleotide sequence of publishing toxin.
Fittle: The complete nucleotide sequence of tetanus toxin.
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Residues: 1-1315 <FAI>
Cross-references: UNIPARC:UP1000003617E; GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g
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A;Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A;Reference number: US0099; MUID:89093918; PMID:2463305
A;Contents: annotation; epitope region
R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.E.
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Residues: 743-1315 <FA2>
Cross-references: UNIPARC:UPI0000156CFA; GB:M12739; NID:g144920; PIDN:AAA23282.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tritle: Isolation, purification, and characterization of fragment B, the NH-2-terminal Reference number: A60759; MUID:90035436; PMID:2478476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C
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Title: Cloning, nuclectide sequencing, and expression of tetanus toxin fragment Reference number: A25194; MUID:86085672; PMID:3510187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::::|||:||::||
1046 DENIDENOMIMIRDFNIFSKELSNEDINIVYEGQILRNVIKDYMGNPLKFDTEYYIINDN 1105
                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                      986 IFDYSESLSHTGYTNKWFFVTITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGI 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 -VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                        1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                               1;
                                                                                                                                       Length 1276;
                                                                                                                                                                                                                                               Indels
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Residues: 865-894 <FA3>
Cross-references: WNIPARC:UPI000017364D
Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozuteumi, K.; Okabe,
Afect. Immun. 57, 3588-3593, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.J.; Allen,
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A,Title: Tetanus and botulinum-B neurotoxins block neurc
A,Reference number: S27125; MUID:93063293; PMID:1331807
                                                                                                                                            DB 2;
                                                                                                                                            ; Score 245.5; DB 2;
; Pred. No. 4.2e-14;
33; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: strain CN3911
Fairweather, N.F.; Lyness, V.A.; Pickard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 461-475 <MAT>
Cross-references: UNIPARC:UP1000017364B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1106 YIDRYİAPESNVLVLVQ 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 RIDKSITONSNFLNING 136
                                                                                                                                       32.3%;
                                                                                                                                                                                                                                                          Conservative
C;Superfamily: tetanus toxin C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 1-1315 <EIS>
                                                                                                                                                       Query Match
Best Local Similarity
Matches 48; Conserv
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R,Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, S.; Kriegla R,Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, S.; Kriegla A,Cleic Acida Res. 18, S556, 1996
A,Title: Nucleotide sequence of the gene encoding Clostridium botulinum neurotoxin type A,Reference number: S11455; MUID:91016853; PMID:2216736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1276 <BIN>
A;Cross-references: UNIPROT:P19321; UNIPARC:UPI0000126B83; EMBL:X54254; NID:940395; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: protein Molecule type: protein Molecule type: protein Molecule 142-459 «SCRAC» Molecule 142-459 «SCRAC» Molecule 142-459 «SCRAC» Molecule 142-459 «SCRAC» Molecule 142-459 «SCRAC» Molecule 156, Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R ature 359, 812-815, 1992 Molecule Molecule 159, 812-815, 1992 Molecule Molecule 162-416 Molecule 162-416 Molecule 163-416 Molecule 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contents: annotation
Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
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C; Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F; 2-441/Product: bontoxilysin B light chain #status experimental <LGHT>
F; 442-1291/Product: bontoxilysin B heavy chain #status experimental <HVY>
F; 230, 234/Alinding site: zinc (His) #status predicted
F; 231/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCND-TRYVGIRYFKVFDTELGKTELFTLYSDEPDPSILKDFWGNYLLYNKRYYLLNL-- 118
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;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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botulinum neurotoxin type D - Clostridium botulinum

A, Status: preliminary, translation not shown A, Molecule type: DNA

A; Accession: S11455

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59; Conservative

Best Local Similarity Matches 59; Conserva

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Appl. Environ. Microbiol. 57, 1168-1172, 1991
Aprille: Cloning of the structural gene for Clostridium botulinum type C-1
A; Reference number: A49777; MUID:91282468; PMID:2059039
A; Accession: A49777
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-607 < TS3>
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botulinum neurotoxin type Dsa precursor - Clostridium botulinum phage d-sA
C;Species: Clostridium botulinum phage d-sA
A;Note: host Clostridium botulinum type D (strain South Africa)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S70582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYLLNLLRTDKSITQNSNFLNINQQR 138
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Dotulinum neurotoxin type C1 precursor - Clostridium botulinum (type C, strain c-st)

C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: D-Mar-1994 #sequence revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S11291; A35396; $22166; A49777
R/Hauser, D.: Eklund, M.W.; Kurazono, H.; Binz, T.; Niemann, H.; Gill, D.M.; Boquet, P.;
Nucleic Acids Res. 18, 4924, 1990
A/Reference number: S11291; MUID:90370487; PMID:2204031
A/Scession: S11291
A/Scession: S11291
A/Scession: S11291
A/Scession: S11291
A/Scession: S11291
A/Scession: S11291
A/Scession: S11291
A/Scession: S11291
A/Scession: A35396
A/Scession: A35396
A/Status: precliminary
A/Molecule type: DNA
A/References: UNIPARC:UP1000016D75D; EMBL:X53751; NID:914905; PIDN
R/Kimura, K.; Fulli, N.; Tsuzuki, K.; Murakani, T.; Indoh, T.; Yokosawa, N.; Takeshi, K.
Biochem: Biophys: Res. Commun. 171, 1304-1311, 1990
A/Reference number: A35396; MUID:91024998; PMID:2222445
A/Accession: A35396
A/Status: precliminary not compared with conceptual translation
A/Residues: 1-669, K.; Kimura, K.; Fulli, N.; Yokosawa, N.; Oguma, K.
R/Fauzuki, K.; Kimura, K.; Fulli, N.; Vokosawa, N.; Oguma, K.
R/Description: Nucleotide sequence of the gene for one of the components of hemagglutini
A/Reference number: A3236;
A/References: UNIPARC:UP1000016709
                                                                                                                                                                                                                                            A/Cross-references: UNIPARC: UPI000017364F
C/Comment: The source of this protein was an extrachromosomal plasmid.
C/Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra dual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C/Comment: Fragment E forms ion channels in a lipid bilayer. Fragment C binds to ganglid C/Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
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A. Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt
A. Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt
C. Superfamily: tetanus toxin
C. Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F. 2457/Product: tentoxylysin light chain (fragment B.C) #status predicted <TLL>
F. 461-1315/Product: tentoxylysin heavy chain (fragment B.C) #status experimental <TTH>
F. 461-1315/Domain: channel forming (fragment B) #status predicted <TXB>
F. 865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>
F. 233,237/Binding site: zinc (His) #status predicted
F. 234/Active site: Glu #status predicted
   R,de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
Eur. J. Biochem. 229, 61-69, 1995
A,Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.
A;Reference number: S69348; MUID:95262688; PMID:7744050
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A/Accession: S22166
A/Accession: S22166
A/Accession: S22166
A/Accession: S22166
A/Accession: S22166
A/Accession: S22166
A/Accession: S22166
A/Residues: 1-1291 <TS2>
A/Residues: 1-1291 <TS2>
A/Cross-references: UNIPARC:UPI0000093F60; EMBL:X62389; NID:g558175; PIDN:CAA44263.1; PI
A/Cross-references: UNIPARC:UPI0000093F60; EMBL:X62389; NID:g558175; PIDN:CAA44263.1; PI
A/Kimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Oguma, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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                                                                                                                                              A;Accession: S69348
A;Molecule type: protein
A;Residues: 2-31 <DEF>
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and its associated non-toxic pa
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R. Hauser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R.
R. Hauser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R.
Mol. Gen. Genet. 243, 531-640, 1994
A.; Title: Organization of the botulinum neurotoxin C1 gene and its associated non-toxic A; Reference number: S46426; MUID:94331293; PMID:8028579
A.; Reference number: S46426; MUID:94331293; PMID:8028579
A.; Residue type: DNA
A.; Residues: 1-1291 cHAU>
A.; Residues: 1-1291 cHAU>
A.; Residues: UNIPROT:Q93HT3; UNIPARC:UP100000B3F60; EMBL:X72793; NID:9516171; B.
A.; Cross-references: UNIPROT:Q93HT3; UNIPARC:UP100000B3F60; EMBL:X72793; NID:9516171; B.
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                                                                                                                                                                                                                                                                                               1052 KIPDTGLITSDSDNINMMIRDFYIFAKELDGKDINILFNSLQYTNVVVDYMGNDLRYNKE 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain C 468
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May C; Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                       GCNDTRYV------GIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N,Alternate names: BoxT/C1 protein
C;Species: Clostridium botulinum phage 1C
A;Variety: strain C 468
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         botulinum neurotoxin C1 - Clostridium botulinum phage 1C (strain C 468)
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                                                                                                                                                                                                       Indels
                                                                                                                                Query Match
31.4%; Score 239; DB 2; L.
Best Local Similarity 37.0%; Pred. No. 1.7e-13;
Matches 54; Conservative 25; Mismatches 57;
A;Cross-references: UNIPARC:UPI000017670A; GB:D90210
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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R.Fujii, N.; Kimura, K.; Yokosawa, N.; Yashiki, T.; Tsuzuki, K.; Oguma, K. J. Gen. Microbiol. 139, 79-86, 1993
A;Title: The complete nucleotide sequence of the gene encoding the nontoxic component of A;Reference number: A47708; MUID:93195515; PMID:8450310
A;Contents: type E, Mashike
A;Accession: A47708
                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-1285 <MOR>
A; Residues: 1-1285 <MOR>
A; Cross-references: UNIPARC:UPI00000B54BA; EMBL:D38442; NID:g1374775; PIDN:BAA07477.1; F C; Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu a disulfide bond. The heavy chain mediates the binding of toxin to the presynaptic membra C; Superfamily: tetanus toxin C; Superfamily: tetanus toxin F; Transmembrane protein F; F; Fyvorduct: botulinum neurotoxin type Dsa light chain #status predicted <MAII> F; H-447/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MAII> F; H-48-1285/Producted <MAII> F; H-48-1285/Producted <MAII> F; H-48-1285/Producted <MAII> F; H-48-1285/Producted <MAII> F; H-48-1285/Pr
R;Moriishi, K.; Koura, M.; Abe, N.; Fujii, N.; Fujinaga, Y.; Inoue, K.; Ogumad, K. Biochim. Biophys. Acta 1307, 123-126, 1996
A;Title: Mosaic structures of neurotoxins produced from Clostridium botulinum types C an A;Reference number: S70582; MUID:96283801; PMID:8679691
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Accession: A47708
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A; Residues: 1-1162 <FUJ>
A; Cross-references: UNIPARC:UP1000017ACE7
A; Note: sequence extracted from NCBI backbone (NCBIN:127249, NCBIP:127250)
C; Superfamily: tetanus toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.6%; Score 225; DB 2; Length 1285; 34.2%; Pred. No. 3e-12; tive 29; Mismatches 57; Indels 1
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Matches 42; Conservative
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## ALIGNMENTS

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                                                                                                                                                                   Name=bont/f; Synonyms=bonT/F;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1278 AA; 147073 MW; A1BE1318431D6918 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elmore M.J., Bodsworth N.J., Whelan S.M., Minton N.P.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X81714; CAA57358.1; -; Genomic_DNA.
EMBL; L35496; AAA23210.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                  Hutson R.A., Collins M.D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:pathogenesis; and peptidolysis; IEA.
                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
BONT/F (Neurotoxin type F);
PRT; 1278 AA
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Neurotoxin.
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InterPro; IPR001095; Peptidase M27.
InterPro; IPR006025; Peptidase M27.
Pfam; PF01742; Peptidase M27; I.
PRINTS; PR00760; BONTOXILYSIN.
  Q57236_CLOBO PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NCTC 10281;
                                                                                                                                                                                                                                                                                          NCBI_TaxID=1491;
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121 TDKSITQNSNFLNINQQRGVYQK 143
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ProDom; PD001963; Botulinum; 1
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NUCLEOTIDE SEQUENCE OF 1-64.
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Matches 113; Conservative 1
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Clostridium botulinum.
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                                        NCBI_TaxID=1561;
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SEQUENCE
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BXF_CLOBO
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                                                                                                                                                                                                                                                                                                       Santos-Buelga J., Collins M.D., East A.K.; "Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B \alpha F
                                                                                                                                                                                       Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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MEDLINE=98440323; PubMed=9767110; DOI=10.1007/s002849900384;
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RGO; GO:0016021; C:integral to membrane; IEA.

RGO; GO:0008405; P:pathospetidase activity; IEA.

RGO; GO:0008405; P:pathospensis; IEA.

RGO; GO:0008508; P:pathospensis; IEA.

RGO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR011591; Botulinum.

RINESPRO; IPR001395; Peptidase_M27.

R PEANYE; PR01742; Peptidase_W27.

R PRINTS; PR00760; BONTOXILYSIN.

R PROSITE; PS001495; AINC PROTEASE; UNKNOWN 1.

R PROSITE; PS001495; AINC PROTEASE; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13631; CAA73972.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
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Last annotation update)
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85.0%; Pred. No. 6.7e-49;
ive 9; Mismatches 12;
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TDKSITQNSNFLNINQQRGVYQKP 1135
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                                                                                09ZAJ5 CLOBO PRELIMINARY;
09ZAJ5 CLOBO (TEMBLE) 10, C
01-MAY-1999 (TYEMBLE) 10, L
01-MAY-1999 (TYEMBLE) 10, L
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01-NOV-1996 (TEMBLEEL 01,
01-NOV-1996 (TEMBLEEL 01,
01-MAR-2004 (TEMBLEEL 26,
Neurotoxin, type F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.03
Matches 119; Conservative
                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                       Clostridium.
NCBI_TaxID=1491;
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61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                          MUCLEOTIDE SEQUENCE.

MEDLINE=93352228; PubMed=8486245; DOI=10.1016/0378-1097(93)90581-L;
Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,
Richardson P.T.;
"Nucleotide sequence of the gene coding for Clostridium barati type F
"Nucleotide sequence of the gene coding for clostridium barati type F
PEMS Microbiol. Lett. 108:175-182(1993).

EMBL; K68262; CAA48329.1; -; Genomic_DNA.

PER; S33411; S33411.
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STRAIN=TYPE F / ATCC 23387;
MEDLINE=93012902; PubMed=1398040; DOI=10.1016/0378-1097(92)90408-G;
East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A.,
Thompson D.E.;
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BoNT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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MEROPS; M27.002; -...

GO; GO:0016021; F:metallopeptidase activity; IEA.

GO; GO:0009405; F:metallopeptidase activity; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

GO; GO:000508; P:proteclysis and peptidolysis; IEA.

InterPro; IPR011591; Botulinum.

InterPro; IPR000505; Peptidase M27.

InterPro; IPR006025; Pepti M. Zn. BS.

Pfam; PP01742; Peptidase M27; I.
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                                  East A.K., Colling M.D.;
"Conserved structure of genes encoding components of botulinum
neurotoxin complex M and the sequence of the gene coding for the
nontoxic component in nonproteolytic Clostridium botulinum type F.";
                                                                                                                                                                     MEDLINE=94013372; PubMed=8408542; Campbell K.D., Collins M.D., East A.K.; Mene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, B, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01742, Peptidase MZ7; 1...
Pfam; PF017953; Toxin_R_bind_N; 1.
Pfam; PF07952; Toxin_trans; 1.
PRINTS; PR00766; BONTOXILYSIN.
PRODOM; PD001963; BOLUlinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botulinum neurotoxin F light chain.
Botulinum neurotoxin F heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S73676; AAC60475.1; -; Genomic_DNA.
X70820; CAA50151.1; -; Genomic_DNA.
X70816; CAA50147.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M92906; AAA23263.1; -; Genomic_DNA
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InterPro; IPR000395; Peptidase M27.
InterPro; IPR012928; Toxin_recpt_bd_
InterPro; IPR012500; Toxin_trans.
                                                                                                                                                                                                                                                                                                               MEDLINE=94230352; PubMed=8175689;
STRAIN=Type F / Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
                                                                                                                 Curr. Microbiol. 29:69-77(1994).
                                                                                                                                                       NUCLEOTIDE SEQUENCE OF: 634-1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'oxin; Transmembrane; Zinc.
                                                                                                                                                                                                                                                                                             IDENTIFICATION OF SUBSTRATE
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S48109; S48109.
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VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92174922; PubMed=1541280; Whelan S.M.; Blmore M.J.; Bardine M.J.; Baddworth N.J.; Atkinson T.; Minton N.P.; "The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                                                                                                                               1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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Bainz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison
"The cher clostridial neurotoxins.";
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Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BXE CLOBU

000496, q45862;

01-JUL-1993 (Rel. 26, Last sequence update)

01-JUL-1993 (Rel. 26, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

13-SEP-2005 (Rel. 48, Last banctation update)

Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BONT/E)

Botulinum neurotoxin E light chain;

----ilvain E) (Contains: Botulinum neurotoxin E light chain;
                       Interchain (between light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Zinc (catalytic) (By similarity)
                                                                                                                                    Length 1274;
                                                                                                                                                                                           14; Indels
                                                                             146710 MW; 5B99756A7438B921 CRC64;
                                                                                                                                       ; DB 1;
4.5e-47;
                                                         (Probable
                                                                                                                                       Score 612; DB
Pred. No. 4.5e-
10; Mismatches
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                                                         chains)
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MEDLINE=92181428; PubMed=1543481;
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Matches 116; Conservative
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  231
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                                                                                      1274 AA;
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Matches
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Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
Jahn R., Niemann H.;
                              **STRAIN=TYPE B / Hazen 36208;
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxin gene and
specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                         MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schlavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Benfenati F., Wilson M.C., Montecucco C.; Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds."; FEBS Lett. 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO076; DONTOXILYSIN.
PRODOM; PRO0761; BONTOXILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
AD-structure; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
INIT_MET 1 421 Botulinum neurotoxin R licht chair
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
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EMBL, X62683; CAA44558.1; -; Genomic_DNA.
EMBL, X70815; CAA50146.1; -; Genomic_DNA.
PIR, S08575; S08575.
PIR, S21178; S21178.
PDB; 1T3A; X-ray; A/B=1-421.
PDB; 1T3C; X-ray; A/B=1-421.
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InterPro; IPR06025; Pept M Zn BS.
InterPro; IPR001395; Pept M Zn BS.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012500; Toxin trans.
Pfam; PF01745; Peptidase MZ7; I.
Pfam; PF07953; Toxin R bind N; I.
Pfam; PF07952; Toxin trans.
                                                                                                                                                                                                          IDENTIFICATION OF SUBSTRATE.
                                                                                                                 IDENTIFICATION OF SUBSTRATE
Biochimie 72:213-217(1990)
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Tsukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T.,
Nakamura S., Karasawa T., Kozaki S.;
Sequence of the botulinum neurotoxin type E.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
       By similarity.

By similarity.

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Interchain (between light and heavy chains) (Probable).

R - 9 (in Ref. 2).

C - S (in Ref. 2) and 3).

R - A (in Ref. 2 and 3).

I -> L (in Ref. 2 and 6).

FE -> LQ (in Ref. 2 and 6).

FE -> LQ (in Ref. 2 and 6).

R -> A (in Ref. 2 and 6).

R -> A (in Ref. 2 and 6).

N -> NN (in Ref. 2 and 6).

N -> NN (in Ref. 2 and 6).
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Botulinum neurotoxin E heavy chain.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulium neurotoxin type B.
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                                                                                                                                                                                                                                                                               DB 1;
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Local Similarity 68.1%; Pred. No. 1.4e-36;
hes 94; Conservative 21; Mismatches 22
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1194 119
1250 AA;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endopeptidase.
-!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
-!- SUBCELLULANE LOCATION: Secreted.
-!- MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
-!- SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yashiki T., Oguma K.; "Itagent encoding the 5'-terminus of the botulinum "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91237316; PubMed=2033376;
Pujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N.,
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 43181, and ATCC 43755;
MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin B derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
13.SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
Ebculinum neurotoxin E heavy chain].
Clostridum butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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STRAIN-5262;
Gimenez J., Poley J., Dasgupta B.R.;
Gimenez J., Foley J., Dasgupta B.R.;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
PASEB J. 2:A1750-A1750(1988).
PASEB J. 2:A1750-A1750(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 183:107-113(1992)
                                                  PRT; 1250 AA
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EMBL; X53100; CAA37321.1; -; Genomic_DNA.
PIR; JH0256; JH0256.
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR000395; Peptidase M27.
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                                                  STANDARD;
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InterPro; IPR006025;
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                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BL6340
                                               BXE CLOBU P30995;
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  RESULT 7

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62 GCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRT 121
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF07953; Toxin R bInd N; 1.
Pfam; PF07952; Toxin RITAINS; 1.
PRINTS; PR00760; BONTOXILISIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00442; ZINC_PROTEASE; 1.
Direct protein sequencing; Hydrolaes; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
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Tsukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T.,
Nakamura S., Karasawa T., Kozaki S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB088207; BAC05434.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                     212 212 By similarity.
213 213 Zinc (catalytic) (By similarity).
214 215 Zinc (catalytic) (By similarity).
417 425 Interchain (between light and heavy chains) (Probable).
229 229 K -> M (in Ref. 2).
229 Ax, 143266 MW; 8171B5B2C2312857 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                           Botulinum neurotoxin E light chain.
Botulinum neurotoxin E heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.1%; Score 495.5; DB 1; Length 1250; 67.4%; Pred. No. 2.1e-36; Live 23; Mismatches 21; Indels 1;
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PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1252 AA; 143510 MW; 41B633BB744D3B41 CRC64;
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008505; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:pathogenessis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR000355; Peptidase M27.
InterPro; IPR00055; Peptidase M27.
InterPro; IPR0142; Peptidase M27.
IPR01142; Peptidase M27; I.
PRINTS; PR0176; BONTOXILYSIN.
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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08 KZMS CLOBU.
D QBKZMS CLOBU PRELIMINARY;
AC Q8 KZMS;
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Matches 93; Conservative
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EMBL; AB03770
HSSP; Q45894;
SMR; Q9K395;
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                                                                        2 FNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV 61
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                                     Gaps
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Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Query Match 65.1%; Score 495.5; DB 2; Length 1252; Best Local Similarity 67.4%; Pred. No. 2.1e-36; Matches 93; Conservative 23; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type E botulinum toxin.
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Q9FAR6;
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Best Local Similarity
Matches 93; Conserva
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974 VFKYGNANGISDYINKWIFVTITNDRLGDSKLYINGHLIDQKSILNLGNIHVSDNILFKI 1033
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STRAIN=LCL 095, LCL 155, KZ 1899, KZ 1897, KZ 1898, KZ 1886, KZ 1887,
KZ 1889, KZ 1890, KZ 1891, and LCL 063;
MEDLINE=20509829; PubMed=11055954;
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Wang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y amakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
"Genetic analysis of type E botulinum toxin-producing Clostridium butyricum strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium butyricum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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2021F4E427070296 CRC64;
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66.9%; Pred. No. 9.1e-36;
iive 22; Mismatches 23;
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                                                                                                             01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-FEB-2005 (TrEMBLrel. 29,
Type B botulinum toxin.
Q9K395_CLOBU PRELIMINARY;
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BXA1_CLOBO
ID BXA1_CLOBO
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Dasgupta B.R., Foley J., Niece R.; "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson D.E., Brehm J.K., Oultram J.D., Swinfield T.-J., Shone C.C., Atkinson T., Melling J., Minton N.P., "The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding
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MEDINE=97016817; PubMed=8863443;
BEST A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
BORTALK. Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
Coganization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
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Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
The complete sequence of bottulinum neurotoxin type A and comparison With other clostridial neurotoxins.";
With other clostridial neurotoxins.";
J. Biol. Chem. 265:9153-9158(1990).
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MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(95)01241-5;
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01-UUL-1989 (Rel. 11, Created)
01-UUL-1983 (Rel. 26, Last sequence update)
01-SRP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-
                                                                                                                                                                                                                                                                                                            Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the N-terminal encoding region.";
Biochem. Biophys. Res. Commun. 162:1388-1395(1989).
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                                                                                                                                                                                                       chain; Botulinum neurotoxin A heavy-chain].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Type A / NCTC 2916;
MEDLINE=90235864; PubMed=2185020;
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                                                                                                                                                                                                                                               Name=botA; Synonyms=atx, bna;
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                                                                                                                                                                                                                                                                                    botulinum.
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HARREN BERTARE REPRESENTARE REP

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Furic. Biol. 5:898-902(1998).
Function: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain from the high chain (L) hydrolyzes the 197-cln-|-Ang-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98455071; PubMed-9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy chain (H).
SUBCELUULAR LOCATION: Secreted.
PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the
treatment of strabismus and blepharospasm associated with dystonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates. COFACTOR: Binds 1 zinc ion per subunit.
                                                                                                                                                                                                               PROTEIN SEQUENCE OF 448-482.
MEDLINE=85285016; PubMed=3896784;
Shone C.C., Hambleton P., Melling J.;
Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94124495; PubMed-8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
Jahn R., Niemann H.;
"Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gimenez J.A., DasGupta B.R.;
"Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72,
"85, 42, and 18 kD fragments.";
J. Protein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; "Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds."; PEBS Lett. 335:99-103(1993).
                                                                                     MEDLINE=89024662; PubMed=3178218;
Sathymoorthy V., Dasgupta B.R., Foley J., Niece R.L.;
"Botulinum neurotoxin type A: cleavage of the heavy chain into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
"Site-directed mutagenesis identifies active-site residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            failure.
CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light chain of botulinum neurotoxin type a.";
Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
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                                                                                                                                                                       Arch. Biochem. Biophys. 266:142-151(1988)
                                                               PROTEIN SEQUENCE OF 448-474 AND 872-895.
terminus and around the nicking site."; Biochimie 72:661-664(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION OF SUBSTRATE.
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1296 AA

PRT;

us-08-981-087b-3.rup

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Q7B8V4 CLOBO PRELIMINARY;
                                                                            Name=bont/a;
                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                               Clostridium
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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BXA2_CLOBO
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  997 VFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKL 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                      R InterPro; IPR01159; Botulinum.
R InterPro; IPR001055; Pept M Zn BS.
InterPro; IPR000305; Pept M Zn BS.
R InterPro; IPR012928; Toxin_recpt_bd_N.
R InterPro; IPR012500; Toxin_trans.
R Pfam; PF0742; Peptidase MZ7; 1.
R Pfam; PF07952; Toxin_trans; 1.
R Pfam; PF07952; Toxin_trans; 1.
R PRINTS; PR00760; BONTOXILYSIN.
R PRODO; PD001963; BCULinum; 1.
R PROSITE; PS00144; ZINC_PROTEASE; 1.
R PROSITE; PS00144; ZINC_PROTEASE; 1.
R MOSITE; PS00145; Bourctoxin; Pharmaceutical; Protease; Toxin;
                                                                                    WWW="http://www.botox.com/site/".
DATABASE: NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;
WWW="http://www.expasy.org/spotlight/back_issues/sptlt019.shtml".
and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                        by abnormal muscle contraction.
MISCELLANEOUS: There are seven antigenically distinct forms of
botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
SIMILARITY: Belongs to the peptidase M27 family.
DATABASE: NAME=BOTOX product information Web site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E->A: Drastic decrease in enzymatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botulinum neurotoxin A light-chain.
Botulinum neurotoxin A heavy-chain.
Potential.
Potential.
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Pred. No. 2.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (catalytic)
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(catalytic)
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Genomic DNA.
Genomic DNA.
Genomic DNA.
Genomic DNA.
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                                                                                                                                                                                                                                              EMBL; D67030; BAA11051.1; -; BMBL; M27892; AAA23269.1; -; PIR; A35294; BTCLAB. PDB; 3BTA; X-ray; A=1-1295. MEROPS; M27.002; -.
                                                                                                                                                                                                           EMBL; X52066; CAA36289.1; -;
EMBL; M30196; AAA23262.1; -;
EMBL; X92973; CAA63551.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.9%;
57.6%;
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261
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222
226
226
453
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METAL
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MUTAGEN
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RESULT 12 Q7B8V4\_CLOBO

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998 VFKYSQMINISDYINRWIFVTITNNRLANSKIYINGRLIDQKPISNLGNIHASNNIMFKL 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Allergan-Hall A;
MEDLINE=22919384; Pubmed=14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zhang L., Lin W.J., Lit S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE=S4413603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
MEDLINE=S4413603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
Willems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridium
botulinum type A associated with infant botulism: comparison with
other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                                                                                                                                   Dineen S.S., Bradshaw M., Johnson B.A.;
"Neurotoxiin gene clusters in Clostridium botulinum type A strains: sequence comparison and evolutionary implications.";
Curr. Microbiol. 46:345-352(2003).
                                                                                                                                                                                                                                                                                                      STRAIN=Hall A-hyper;
MEDLINE=22617869; PubMed=12732962; DOI=10.1007/800284-002-3851-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q45894; P77780; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2005 (Rel. 41, Last amotation update) 28-FIB-2005 (Rel. 48, Last amotation update) 28-FIB-2005 (Rel. 48, Last amotation update) 38-FIB-2005 (Rel. 48, Last amotation update) 38-FIB-2005 (Rel. 48, Last amotation Recursor (RC 3.4.24.69) (BoNT/A) (Boncoxilyain A) (BOTOX) [Contains: Botulinum neurotoxin A heavy-chain].
                                                                                                                                       Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=botA; Synonyms=atx, bna;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1296 AA; 149425 MW; DEA8CF2754AE43E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium botulinum type A-Hall (Allergan) strain.";
Gene 315:21-32(2003).
EMBL; AEGE1540; AAA75961.1; -; Genomic_DNA.
EMBL; AF488749; AAQ06331.1; -; Genomic_DNA.
                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.9%; Score 440.5; DB 2 57.6%; Pred. No. 2.3e-31; iive 26; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1295 AA
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        Created)
10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                  BONT/A (Neurotoxin BoNT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                      NCBI_TaxID=1491;
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                                                    East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding
components of the boullinum toxin complex in proteolytic clostridium
types A, B, and F: avidence of chimeric sequences in the
botulinum types A, B, and F: avidence of chimeric sequences in the
gene encoding the nontoxic nonhemagglutinin component.";
In J. Syst. Bacteriol. 46:1105-112(1996).
In ThyCION: Inhibits acetyloholine release.
The C-terminus of the niternalized by receptor-mediated endocytosis.
The C-terminus of the heavy chain (H) is responsible for the
adherence of the toxin to the cell surface while the N-terminus
mediates transport of the light chain from the endocytic vesicle
to the cytosol. After translocation, the light chain (L)
hydrolyzes the 197-Gln-[-Arg-198 bond in SNRP-25, thereby blocking
neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                             CATALTTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity).
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1D-structure; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin;
                                                                                                                                                                                                                                                                                            results in flaccid paralysis, with frequent heart or respiratory failure (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANBOUGS: There are seven antigenically distinct forms botulinum neurotoxin: Types.A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Zinc.

0 By similarity.
47 Botulinum neurotoxin A light-chain.
1295 Botulinum neurotoxin A heavy-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heav
chains) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.7%; Score 423.5; DB 1; Length 1295; 56.9%; Pred. No. 8.4e-30;
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fw; SDA04A13D98D6372 CRC64;
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Potential.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF07953; Toxin_R_bind_N; 1.
Pfam; PF07952; Toxin_trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1E1H; X-ray; A/C=9-249, B/D=250-415.
MEROPS; M27.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X73423; CAA51824.1; -; Genomic_DNA.
EMBL; X87974; CAA61234.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR006025; Pept M Zn BS.
InterPro; IPR000395; PeptIdase M27.
InterPro; IPR012928; Toxin_recpt_bd
InterPro; IPR012500; Toxin_trans.
                                             MEDLINE=97016817; PubMed=8863443;
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226
453
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLINLL
                                                                                                                                                                                             1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                          VGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type A2 botulinum neurotoxin.
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1296 AA; 149410 MW; 6F12E7BF28ED69D1 CRC64;
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Botulinum neurotoxin type B (Fragment).
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Q9X708;
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23; Mismatches

Conservative

Best Local Similarity Matches 82; Conserv

Query Match

Indels

NCBI\_TaxID=1491;

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62 GCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLINL-- 118
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                                                                                                                                                                                                                                                                                                                                                                                                           2 PNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV 61
             N (1) —

NUCLECTIDE SEQUENCE.

MEDLINE-9343691; PubMed=104413679;

MEDLINE-9343691; PubMed=104413679;

A Lalli G., Herreros J., Osborne S.L., Montecucco C., Rossetto O., Schiavo G.;

A Schiavo G.;

I "Functional characterisation of tetanus and botulinum neurotoxins in funding domains ";

J. Cell Sci. 112:2715-2724(1999).

I. Cell Sci. 112:2715-2724(1999).

REMBL; AJ245628; CAB43706.1; -; Genomic_DNA.

RISSP; P106444; LEPW.

RISSP; P106444; LEPW.

ROJ; GO:0009405; P:pathogenesis; IEA.

N Neurocoxin.
                                                                                                                                                                                                                                                                                                                                Query Match

39.6%; Score 301; DB 2; Length 441;
Best Local Similarity 39.9%; Pred. No. 4.1e-19;
Matches 63; Conservative 30; Mismatches 43; Indels 22; Gaps
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441 441
441 AA; 52772 MW; 721D0B468E8C95A4 CRC64;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein Run on:

March 2, 2006, 00:46:47; Search time 17.7077 Seconds (without alignments) 672.325 Million cell updates/sec

US-08-981-087B-3 761 1 VFNYTQMISISDYINKWIFV.....ITQNSNF1NINQQRGVYQKP 144 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

572060 seqs, 82675679 residues Searched:

572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptcdata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptcdata/1/iaa/RE\_COMB.pep:\*
/cgn2\_6/ptcdata/1/iaa/RE\_COMB.pep:\* Issued Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		de			COLUMNIC	
Result No.	Score	Query Match	Length	DB	ID	Description
-	440.5	57.9	382	7	US-09-288-326A-9	Sequence 9, Appli
7	440.5	57.9	382	~	US-09-548-409B-9	o,
m	440.5	57.9	438	Н	US-08-480-604A-23	23,
4	440.5	57.9	438	Н	US-08-405-496A-23	23,
ഗ		57.9	438	~	US-08-915-136-23	23,
9	440.5	57.9	438	~	US-09-084-517-23	23,
7	440.5	57.9	462	Н	US-08-480-604A-26	26,
œ	440.5	57.9	462	Н	US-08-405-496A-26	26,
6	440.5	57.9	462	~	US-08-915-136-26	26,
10	440.5	57.9	462	7	US-09-084-517-26	Sequence 26, Appl
11	440.5	57.9	1296	٦	US-08-480-604A-28	28,
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13	440.5	57.9	1296	~	US-08-915-136-28	28,
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16	284.5	37.4	1169	~	US-09-255-829-20	20, 7
17	284.5	37.4	1290	~	US-10-360-101-220	220,
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19	240.5	31.6	452	Н	US-07-618-312A-4	4,
20	240.5	31.6	452	Н	US-08-280-228-2	'n
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23	240.5	31.6	853	~	US-08-913-880C-17	17,
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27	240.5	31.6	865	~	US-08-913-880C-13	Sequence 13, App]

Sequence 9, Application US/09548409B
Patent No. 684399B
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Sachs, George
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treament of Pancreatitis
FILE REFERENCE: 17282CIP(AP)

US-09-548-409B-9

TITLE OF INVENTION: Treament of Pancreatitis FILE REFERENCE: 17282CIP(AP) CURRENT APPLICATION NUMBER: US/09/548,409B

Sequence 12, Appl Sequence 11, Appl Sequence 10, Appl Sequence 14, Appli Sequence 14, Appli Sequence 10, Appl Sequence 18993, A Sequence 62, Appli Sequence 62, Appli
US-08-913-880C-12 US-08-913-880C-11 US-08-913-880C-10 US-08-913-880C-10 US-08-911-786A-8 US-09-248-796A-14679 US-09-248-796A-10 US-08-915-136-10 US-08-915-136-10 US-08-915-136-10 US-08-915-136-10 US-09-917-136-10 US-09-917-10 US-09-084-517-10
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### ALIGNMENTS

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84 VFKYSQMINISDYINRWIFVTITINNRLANSKIYINGRLIDQKPISNLGNIHASNNIMFKL 143
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                                                                                             APPLICANT: Aoki, K. Roger
APPLICANT: Sachs, George
ITILE OF INVENTION: Methods and Compositions for the
ITILE OF INVENTION: Treatment of Pancreatitis
FILE REFERENCE: 17282
CURRENT APPLICATION NUMBER: US/09/288,326A
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 9
IENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%; Score 440.5; DB 2; ilarity 57.6%; Pred. No. 2.4e-42; Conservative 26; Mismatches 30;
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               Sequence 9, Application US/09288326A
Patent No. 6776590
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Clostridium Botilinum US-09-288-326A-9
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 83; Conserv
-09-288-326A-9
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08480604A

Sequence 23, Application US/08480604A

Patent No. 5736139

GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFCAD, ONGIAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER MEDIENE & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATE:
ZIP.
                                                                                                                                                                                                                                                                  Query Match

57.9%; Score 440.5; DB 2; Length 382;
Best Local Similarity 57.6%; Pred. No. 2.4e-42;
Matches 83; Conservative 26; Mismatches 30; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-UCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-UN-1995
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/45,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1994
FILING DATE: 02-DEC-1993
FILING DATE: 04-DEC-1993
FILING DATE: 04-DEC-1993
FILING DATE: 04-DEC-1993
FILING DATE: 04-DEC-1993
                    PRIOR APPLICATION NUMBER: US 09/288,326 PRIOR FILING DATE: 1999-04-08 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PASESEQ for Windows Version 3.0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT FILING DATE: 2000-04-13
                                                                                                                                                                       TYPE: PRT ORGANISM: Clostridium botulinum
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                                                                                                                                                                                                                     US-09-548-409B-9
                                                                                                                    SEQ ID NO 9
LENGTH: 382
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140 VFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKL 199
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US-08-105-496A-23
Sequence 23, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: WACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: WERROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE MEDIENK & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
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APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION NUMBER: US/08/405,496A
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/329,154
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 04-DEC-1992
ATTONING APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: DATA:
APPLICATION NUMBER: US 07/429,791
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Best Local Similarity 57.6%; Pred. No. 2.9e-42;
Matches 83; Conservative 26; Mismatches 30
                                                                             NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMONICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 RTDKSITQNS----NFLNINQQRG 139
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US 07/429,791
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                                                                                                                                                                                                                                                                       TOPOLOGY: 1130 amino acids
TYPE: amino acid
TOPOLOGY: 11000
                          FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-480-604A-23
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STATE: CALIFORNIA
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-084-517-23
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS CARROLL, LLP
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 222 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                              Query Match 57.9%; Score 440.5; DB 1; Length Best Local Similarity 57.6%; Pred. No. 2.9e-42; Matches 83; Conservative 26; Mismatches 30; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
REGISTRATION NUMBER: 40,027
REPERBNICH/DOCKET NUMBER: OPHD-01308
FELECOMMUNICATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
OPOLOGY: linear
MOLECULE TYPE: protein
US-08-405-496A-23
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FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
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02-DEC-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 02-DEC-19
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CALIFORNIA
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APPLICANT: KINK,
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140 VFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKL 199
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Patent No. 6613329

GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 438;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NATR:
APPLICATION NUMBER: US/09/084,517
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57.6%; Pred. No. 2.9e-42;
tive 26; Mismatches 30
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STREET: 220 MONTGOMERY STREET, SUITE 2200
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 DPNKYVDVNNVGIRGYMYLKGPRG 283
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
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25-OCT-1994
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                                                                                                                                                                                                                            TELEFAX: (415) 397-838
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 16-MAR-1995
04-DEC-1992
                                                                                                                                                                                                                                                                                                           438 amino acids
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Best Local Similarity 57.00
"Thos 83; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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APPLICATION NUMBER: 1
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-915-136-23
                                                                                                                                                                                                                                                                                                                                   amino acid
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US-08-480-604A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 DGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLY 259
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; Sequence 26, Application US/08480604A
; Patent No. 2736139
; GENERAL INFORMATION;
APPLICANT: KINK, JOHN A.
; APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
; APPLICANT: PATERFORD, DOUGLAS C.
; TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
; TUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
ADDRESSE: MEDIEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.9%; Score 440.5; DB 2; Length Best Local Similarity 57.6%; Pred. No. 2.9e-42; Matches 83; Conservative 26; Mismatches 30; Indels
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ZIP: 94104

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,604A

"TITING DATE: 07-210-1995
PILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01610
TELEPHONE: (415) 705-8410
TELEPAK: (415) 397-838
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acid
TYPE: amino acid
TYPE: APPLICATION THEAT
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APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
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                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-084-517-23
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61 VGCNDT-RYVGIRYFKVFDTBLGKTBIBTLYSDBPDPSILKDFWGNYLLYNKRYYLLNLL 119
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APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUFOTOXIN
ITILE OF INVENTION: NEUFOTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A FILING DATE: 16-MAR-1995 CLASSIFICATION NUMBER: US/08/405,496A FILING DATE: 25-OCT-1994 PRIOR APPLICATION NUMBER: US/08/329,154 FILING DATE: 25-OCT-1994 PRIOR APPLICATION NUMBER: US/08/329,154 FILING DATE: 25-OCT-1994 PRIOR APPLICATION NUMBER: US/08/161,907 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.9%; Score 440.5; DB 1; Best Local Similarity 57.6%; Pred. No. 3.1e-42; Matches 83; Conservative 26; Mismatches 30;
                                                        PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/985,321

PRIOR APPLICATION NUMBER: US 07/985,321

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/429,791

PILING DATE: 31-0CT-1989

ATTORNEY/AGENT INFORMATION:

NAME: INGOLIA, DIANE E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: 09HD-01763

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NOWBER: 09HD-01763

TELECOMMUNICATION NOWBER: 09HD-01763

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TELECOMMUNICATION NOWBER: 09HD-01763
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ZIP: 94104
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0 '
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/08405496A
Patent No. 5919665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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TOPOLOGY: linear
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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JS-09-084-517-26

JS-09-084-517-26

JEDICAL INFORMATION:

APPLICANT: WILLIAMS, JOHN A.

TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE

NUMBER OF SEQUENCES:

ADDRESSER: HAVERSTOCK, MEDLEN & CARROLL

STREET: 220 MONTGOMENY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;; Score 440.5; DB.;; Pred. No. 3.1e-42, 26; Mismatches 30
                                                                         PRIOR APPLICATION DATE: 25-OCT-1594
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 0.010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/084,517
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                                                         25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.6%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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APPLICATION NUMBER: 1
. FILING DATE: 16-MAR-1
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MOLECULE TYPE: protein
US-08-915-136-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KINK, JOHN A.
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, USHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSEE: ADDRESSEE: ADDRESSEE: SAN MEDLEN & CARROLL, LLP STREET; SAN FRANCISCO CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 462;
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REGISTRATION NUMBER: 40,027
REFERENCE/COCKET NUMBER: 0PHD-01308
TELECOMUNICATION INFORMATION:
TELEFRONE; (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 RIDKSITONS----NFLNINQQRG 139
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
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Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-405-496A-26
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APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PRACH, ORSEPH N.
APPLICANT: PIRCA, JOSEPH N.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
MEDIUM TYPE: PLOPPY disk, CARROLTS TO MONTGOMERY FRANCISCO
STATE: PROPER PROPER PROPER PROPER PROPER PROPER PROPER PROPER PROPER PROPER PROPER PROPER PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROP
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Social Similarity 57.6%; Pred. No. 3.1e-42;

Matches 83; Conservative 26; Mismatches 30; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTOWNEY, ANGERT ATTOWNEY, ATTOWNEY, ANGERT ATTOWNEY, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 0PHD-01610
TELECOMMUNICATION INFORMATION:
TELEFONE (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
                                                                                                                                                                       APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
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; Patent No. 5736139
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 28, Application US/08405496A; Patent No. 5919665; GENERAL INFORMATION:
; PATENTEAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM; ITLLE OF INVENTION: NEUROTOXIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MADDRESS:
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.9%; Score 440.5; DB 1; Best Local Similarity 57.6%; Pred. No. 1.3e-41; Matches 83; Conservative 26; Mismatches 30;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
                                PRICE DATE: 14-AFF-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRICE APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989
ATTORNEY APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|: |: |: |1118 DPNKYVDVNNVGIRGYMYLKGPRG 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                 FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-480-604A-28
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.9%; Score 440.5; DB 2; Length 1296; 57.6%; Pred. No. 1.3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Mismatches
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
APPLICATION NUMBER: US 07/429,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : : | : | : | 1118 DPNKYVDVNNVGIRGYMYLKGPRG 1141
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09084517
Patent No. 6613329
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: HAVERSTOCK,
STREET: 220 MONTGOMERY
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.6'
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-915-136-28
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US-09-084-517-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADINES, NISHA V.
APPLICANT: PRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 57.9%; Score 440.5; DB 1; Length 1 Similarity 57.6%; Pred. No. 1.3e-41; 83; Conservative 26; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                            PAPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA: US 08/161,907
APPLICATION DATA: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA: US 07/429,791
APPLICATION NUMBER: US 07/429,791
RIGHT MACHENIA DATA: NFORMATION:
NAMME: INFORMATION:
NAMME: INFORMATION:
REGISTRATION NUMBER: 40,0077
REGISTRATION NUMBER: 40,0077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08915136
Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: OF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
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Gaps 5,

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610 DGCRDPRRYIMIKYFNLFDKELNBKEIKDLYDSQSNSGILKDFWGNYLQYDKPYYMLNLF 669
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                                                                                                                                                                                                                              1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                       Query Match 55.7%; Score 423.5; DB 2; Length 848; Best Local Similarity 56.9%; Pred. No. 6.6e-40; Matches 82; Conservative 23; Mismatches 34; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RIDKSITQNSNFLNINQQRGVYQK 143
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Job time : 18.7077 secs
                  US-10-360-101-219
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Pacent No. 686126

GENERAL INFORMATION:
APPLICANT: Methouts, Cornelis J.
APPLICANT: Leenhouts, Cornelis J.
TITIE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way TILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT PILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin Version 3.1
SEQ ID NO 219
LENGTH: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
PEATURE:
OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998 VFKYSOMINISDYINRWIFVTITINNRLINNSKIYINGRLIDQKPISNLGNIHASNNIMFKL 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995

PRIOR APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 01-0CT-1989
ATTORNEY AGENT INPORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
RELECHONE: (415) 705-8410
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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Best Local Similarity
Matches 83; Conserva
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Sequence Sequence Sequence Sequence

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Sequence Sequence

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Sequence 3. Application US/08981087A

Publication No. US20020081304A1

GENERAL INFORMATION:

APPLICANT: Mauchline, Margaret L.

APPLICANT: Matchine, Margaret L.

APPLICANT: Tibball Richard W.

TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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1100 No. US20020081304Alth Glebe Rd.
                                                                                                                                                       US-11-001-241-71
US-09-910-186A-14
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                                                                                                                                                                                                                                                                                          ALIGNMENTS
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APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
RECORD APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9511909.5
PILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
                                                                                                                                                                                      US-10-354-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 124-688
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-981-087A-3
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STRANDEDNESS
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                                                                                                    March 2, 2006, 01:11:03 ; Search time 57.2993 Seconds
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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-10-130-973A-14
-10-478-516-23
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US-10-478-516-5
US-10-478-516-6
US-10-478-516-6
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US-10-205-516-12
US-10-205-516-26
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US-10-130-973A-4
US-10-130-973A-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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. Sequence 34, Application US/09910186A
. Publication No. US20030009025A1
. GENERAL INFORMATION:
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                                                                                                                               1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
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                                                         Gaps
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       Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Elmore, Michael J.
APPLICANT: Mauchline, Margaret L.
APPLICANT: Manchine, Margaret L.
APPLICANT: Manchine, Nigel P.
APPLICANT: Pasechnik, Vladimir A.
APPLICANT: Titball, Richard W.
TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20020081304Alth Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 431;
                                                    0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMFOURE: PACENTIN Release #1.0, Version #1.30
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-UN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511909.5
FILING DATE: 12-UN-1996
ATTIANG PAGENT INFORMATION:
NAME: CTAMFORMATION:
NAME: CTAMFORMATION:
NAME: CTAMFORMATION:
NAME: CTAMFORMATION NAME:
  100.0%; Score 761; DB 2;
100.0%; Pred. No. 8.5e-71;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        TDKSITQNSNFLNINQQRGVYQKP 144
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REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 amino acids
Query Match
Best Local Similarity 100.
Matches 144; Conservative
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US-08-981-087A-1
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61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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100.0%; Score 761; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 144; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROTOTIN
TITLE OF INVENTION: NEUROTOTIN
FILE REFERENCE: A336.26-A 06725.0107
CURRENT PILING DATE: 2001-07-20
PRIOR PELICATION NUMBER: DCT/US00/12890
PRIOR PELICATION NUMBER: DCT/US00/12890
PRIOR PELICATION NUMBER: 09/611,419
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR PELING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: 06/133,865
PRIOR FILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
PRIOR PELICATION NUMBER: 60/133,866
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
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PRIOR PILING DATE: 1999-05-12
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PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1993-09-21
NUMBER: OF SEQ ID NOS: 34
SOFTWARE: PRESEQ for Windows Version 4.0
LENGTH: HANDER TO THE TOWN TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWER TOWE
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APPLICANT: Sutton, John
APPLICANT: Stiman, Nigel
TITLE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: US/200-10-21
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PACHELIAN OF SEQ ID NOS: 18
LENGTH: 645
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Publication No. US20040208889A1
GENERAL INFORMATION:
APPLICANT: Sutron, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REPERBINE: 1581:1000000
CURRENT APPLICATION NUMBER: US/10/478,516
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                   Indels
; Pred. No. 3.4e-70; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10130973A Publication No. US20030147895A1 GENERAL INFORMATION: APPLICANT: Shone, Clifford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
  100.08;
Best Local Similarity 100.0
Matches 144; Conservative
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Best Local Simi
Matches 144;
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US-10-478-516-5
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APPLICANT: Park, Jung-Beak
APPLICANT: Maksymowych, Andrew
TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-9601
CURRENT APPLICATION NUMBER: US/10/452,024
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VGCNDTRYVGIRYFKVFDTBLGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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  TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM IITLE OF INVENTION: NEUROFOXIN
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Pred. No. 3.4e-70;
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                                                            FILE KEFERGES A35.6—A 05.25.0107
CURRENT PEDLICATION NUMBER: US/09/910,186A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/US00/12890
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-07-06
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
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100.0%; Score 761; D
Best Local Similarity 100.0%; Pred. No. 3.4
Matches 144; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/123,975
PRIOR FILING DATE: 1993-09-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Construct US-09-910-186A-34
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                                                    FILE REFERENCE: A33626-A 067252.0107
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Sequence 178, Application US/10452024
Publication No. US20040013687A1
GENERAL INFORMATION:
APPLICANT: Simpson, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/133,873
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 178
ISNGTH: 432
TYPE: PRT
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sequence 7, Application US/10130973A

sequence 7, Application WS/10130973A

publication No. US20030147895A1

GENERAL INFORMATION:
APPLICANT: Shone, Clifford
APPLICANT: Staten, John
APPLICANT: Staten, John
APPLICANT: Staten, Wigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920040404

FILE OF INVENTION NUMBER: US/10/130,973A

CURRENT FILING DATE: 2002-10-21

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.0

SEQ ID NO 7

LENGTH: 685
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US-10-478-516-7
  Sequence 7, Application US/10478516;
Publication No. US20040208889A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sutton, John M.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.100000
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT APPLICATION NUMBER: US/10/478,516
FRIOR FILING DATE: 2002-05-21
FRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 7.
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100.0%; Score 761; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.1e-70;
Matches 144; Conservative 0; Mismatches 0;
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Pred. No. 5.8e-70;
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100.0%; Score 761; D
Best Local Similarity 100.0%; Pred. No. 5.8
Matches 144; Conservative 0; Mismatches
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US-10-478-516-6
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APPLICANT: Shone, Clifford C.
TILLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins FITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins FILE REFERENCE: 1581.1000000 CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR PLING DATE: 2000-05-21
PRIOR PPLICATION NUMBER: GB 0112687.9
RNIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 657
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                                                                                                                                                                                                                                       ; OTHER INFORMATION: diphtheria toxin translocation domain with BoNT/F-HC US-10-478-516-5
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Best Local Similarity 100.0%; Score 761; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 144; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                             Length 645;
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Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 144; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2002-05-21
PRIOR PEDLICATION NUMBER: GB 0112687.9
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 645
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                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial sequence
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CTHER INFORMATION: Protein sequence for YopT, factor Xa linker, diphtheria toxin, CTHER INFORMATION: translocation; CTHER INFORMATION: domain, with BONT/F-HC US-10-478-516-26
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APPLICANT: Shone, Clifford C.
APPLICANT: Shone, Clifford C.
APPLICANT: Shone, Clifford C.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins FILE REFERENCE: 1581.1000000
CURRENT APPLICATION NUMBER: US/10/478,516
PRIOR APPLICATION NUMBER: CT/GB02/02384
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR PILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
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100.0%; Pred. No. 9.5e-70;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                           Length 887;
                                                                                                                                                                                                                                                                                      Score 761; DB 4;
Pred. No. 8.4e-70;
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Best Local Similarity 100.0%; Pred. No. 8.4
Matches 144; Conservative 0; Mismatches
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Publication No. US20040208889A1
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: GB 0086;
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 887
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ORGANISM: Artificial sequence
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Matches 144; Conservative
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LENGTH: 979
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APPLICANT: Shone, John
APPLICANT: Shone, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 862
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Publication No. US20030147895A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Shone, Clifferd
APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERBNCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: CT/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
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1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60

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Search completed: March
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                                                                                     Sequence 15, Application US/10130973A

PUBLICATION NO. US20030147895A1

GENERAL INFORMATION:
APPLICANT: Sinone, Clifford
APPLICANT: Sinone, Clifford
APPLICANT: Sinone, Constructs for Delivery of Therapeutic Agents to Neuronal Cells
ITTLE REFERENCE: 1581.092000
ITTLE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Petentin version 3.0
SEQ ID NO 15
LENGTH: 1032
ITYPE: PRI
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| Sequence 14, Application US/10130973A
| Sequence 14, Application US/10130973A
| Sequence 14, Application No. US2003147895A1
| Publication No. US2003147895A1
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
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| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| PRIOR FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2000-12-04
| PRIOR FILING DATE: 2000-12-04
| PRIOR FILING DATE: 2000-12-04
| PRIOR FILING DATE: 1999-12-02
| PRIOR FILING DATE: 2000-04-07
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100.0%; Score 761; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 1e-69;
Matches 144; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 761; DB 4; Length 1092;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 144; Conservative 0; Mismatches 0; Indels 0
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; ORGANISM: Clostridium botulinum
US-10-130-973A-14
RESULT 14
US-10-130-973A-15
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RESULT 1
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1 VFNYTQMISISDYINKWIFV.....ITQNSNFLNINQQRGVYQKP 144
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO3_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO3_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO3_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Sequence 5, Appli	Sequence 8, Appli	Sequence 28, Appl	26,	Sequence 18, Appl	Sequence 3, Appli	,	Sequence 30, Appl	Sequence 20, Appl	Sequence 4, Appli	٦,	Sequence 20, Appl	Sequence 24, Appl	Sequence 141, App	22,	¥	2939,	Sequence 2941, Ap	N	Sequence 2945, Ap	٥,	ì	'n	~	Seguence 420, App
	Desca	Seq	Sed	Segn	Seq	Segr	Sed	Sed	Sed	Sed	Sed	Seg	Seq	Seg	Seq	Sed	Seq	Seq	Sed	Seq	Seq	Sed	Sed	Sed	Sed	бəs
SUMMERTES	ΩI	US/11/062	US/11/062	US-10-909-769-28	US-10-909-769-26	US-10-909-769-18	US/11/062	US/11/062	US-10-909-769-30	US-10-909-769-20	US/11/062	US/11/062	US-11-077-550-20	US-10-909-769-24	US-11-077-550-141	US-10-909-769-22	US-11-051-453-42	US-11-129-741-2939	US-11-129-741-2941	US-11-129-741-2943	US-11-129-741-2945	US-11-129-741-2949	US-11-129-741-2951	US-11-129-741-4245	US-10-895-064-420	US-11-129-741-420
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d	Query Match	100.0	100.0	80.4	65.4	57.9	57.9	57.9	39.0	38.9	37.4	37.4	37.4	32.3	31.6	31.4	11.7	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1
	Score	761	191	612	497.5	440.5	440.5	440.5	296.5	296	284.5	284.5	284.5	245.5	240.5	239	89	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5
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293 365 107			240, 4284, 216, 2351, 2	200, 7 2330, 3028, 8258,	10448, A 5, Appli
Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
US-11-129-741-2937 US-11-129-741-3655 US-11-098-686-10796	US-10-926-709-2 US-10-926-709-7 US-11-129-741-2947 US-10-926-709-8	US-11-098-686-10150 US-11-087-099-2275 US-11-052-554A-230	US-11-052-554A-240 US-11-087-099-4284 US-10-485-517-216 US-10-485-517-351	US-10-485-517-200 US-11-087-099-2330 US-11-087-099-3028 US-11-087-099-8258	US-11-087-099-10448 US-10-959-322-5
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1351 1385 360	302 302 1351 302	1089 369 448	140 342 567 743	326 326 326 326	330
9.6 8.6 7.	9 9 9 9	0 0 0 7 4 6.	9 9 9 9 6 4 6 6	90000	1.6
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			Length 1059; Indels 0	VENYTOMISISDYINKWIFVTITNNRLCNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 	VGCNDTRXVGIRXFKVPDTELGKTEIETLXSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 	
. a ge		from		LIDE LIDE		
smut		gos	DB 7; 9e-67	INGN INGN	PDPS      PDPS	
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oxid 2,471	o,	sing	core 761; red. No. 1. Mismatches	SLGN SLGN	IETL IETL	144 916
11A es Superoxide Dismutase 1/062,471A .,050	1282	nprin	Score 761; DB 7; Pred. No. 1.9e-67; Mismatches 0;		SKTE SKTE	
24 rl 222 331 311	FILING DATE: 1999-11-05 APPLICATION NUMBER: GB 9824282.9 FILING DATE: 1998-11-05 OF SEQ ID NOS: 11 NE: PatentIn Ver. 2.1 NO 5 H: 1059	IIEE: FK1 PEATURE: OTHER INFORMATION: Construct comprising Mn-SOD from B. 1/062,471A-5	0;		OTEL 	TDKSITQNSNFLNINQORGVYQKP                   TDKSITQNSNFLNINQORGVYQKP
1 US/110624 2255093A1 fford charl sha Mark shasam igel Milvery of 800001 MBER: US/1 2005-02-22 BER: 09/831 99-11-05	2.1 2.1	Sequence	100.0%; 100.0%; ive	INKW	FKVF]       FKVF]	
tion No. US20050255093A: tion No. US20050255093A: INCORMATION: ANT: SHONE, Clifford Ch. ANT: SHONE, Clifford Ch. ANT: HALLIS, Bassam ANT: HALLIS, Bassam ANT: SILMAN, Nigel OF INVENTION: Delivery (SFERENCE: 1581.0800001 T APPLICATION NUMBER: US TFILING DATE: 2005-02 APPLICATION NUMBER: 09/ FILING DATE: 1999-11-05 APPLICATION NUMBER: PCT	FILING DATE: 1999-11-05 APPLICATION NUMBER: GB FILING DATE: 1998-11-05 OF SEQ ID NOS: 11 NE: PatentIN Ver. 2.1 NO 5 H: 1059	Sec Const	100 larity 100 Conservative	ISDY.	SIRY 	NATURA NATURA NATURA
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e 5, Application 11 tion No. US2005 Ition No. US2005 ANT: SHONE, Cliant Surrow, 2 ANT: SULLIS, EEFRENCE: 1581. T APPLICATION NO. TELLING DATE: APPLICATION NO.	NG DAIE: 1999- ICATION NUMBER SEQ ID NOS: 11 PatentIn Ver.	Artificial NRMATION: Cc	:=	TYN:	SCENE CONTROL	DKSI      DKSI
5, Ap INFORM WT: SH WT: SH WT: S WT: H WT: B FILIN FILING FILING	LING LICA SEC Pat 1059	I: AX IFORN	ch 11 Sim 144;	1 VI	61 VC 833 VC	121 TI   893 TI
PATE GARAGE TE	RIOR FILLING RIOR APPLICA RIOR FILLING UMBER OF SEQ OFTWARE: Pat. Q ID NO 5 LENGTH: 1059	IIEE: FRI ORGANISM: FEATURE: OTHER INFO	Matc loca]	7		7 8
US/11/062 Sequence 5, Application US/1106 Publication No. US20050255093A1 GENERAL INFORMATION: APPLICANT: SHONE, Clifford Cha APPLICANT: SUTTON, John Mark APPLICANT: HALLIS, BASSEM APPLICANT: SILMAN, Nigel TITLE OF INVENTION: Delivery of FILE REFERENCE: 1581.0800001 CURRENT FILING DATE: 2005-02- PRIOR APPLICATION NUMBER: 09/ PRIOR APPLICATION NUMBER: 09/ PRIOR FILING DATE: 1999-11-05 PRIOR APPLICATION NUMBER: 10/ PRIOR APP	PRIOR FILL PRIOR APPI PRIOR FILI NUMBER OF SOFTWARE: SEQ ID NO 5 LENGTH: 1	; IIFE: FKI ; ORGANISM: Ar ; FEATURE: ; OTHER INFORM US/11/062,471A-5	Query Match Best Local Matches 14			
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APPLICANT: Steward, Lance E.
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Rei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteriss
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteriss
TITLE OF INVENTION: 10xin Compounds with Enhanced Membrane Translocation Characteriss
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18
LENGTH: 849
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APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLEGO10-100 (RO12003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 2 26
LENGTH: 829
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                                                                                                                                                                                                                                           121 TDKSITQNSNFLNINQQRGV 140
                                                                                                                                                                                                                                                                                        678 KDKYITLNSGILNINQQRGV 697
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Publication No. US20060024331A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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US-10-909-769-18
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Sequence 28, Application US/10909769

Sequence 28, Application US/10909769

Sequence 28, Application Occupation Oc
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                                                                                                                   APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
I TITLE CARLIS, Bassam
I TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
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PRIOR PLING DATE: 1998-11-05
PRIOR PLING DATE: 1998-11-05
SPRIOR PLING DATE: 1998-11-05
SEQ ID NOS: 11
SQC ID NOS: 11
SQC ID NOS: 11
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82.9%; Pred. No. 8e-53;
tive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDKSITONSNFLNINOORGVYOKP 941
Sequence 8, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
                                                                                                     APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 82.9%
Matches 116; Conservative
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Best Local Similarity 100.
Matches 144; Conservative
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1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60

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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human Mr
US/11/062,471A-6
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APPLICANT: Fernands Seter
APPLICANT: Fernands Seter
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: Toxin (RO12003-146)
CURRENT PAPLICATION NUMBER: US/10/909, 769
CURRENT PILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30
LENGTH: 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: STIMAN, Nigel.
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Celle
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Celle
FILE REFERENCE: 1581.0800.02.471A
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1005-02-22
PRIOR PELICATION NUMBER: PCF/GB99/03699
PRIOR PELICATION NUMBER: PCF/GB99/03699
PRIOR PLILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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39.0%; Score 296.5; DB 6;
Best Local Similarity 49.6%; Pred. No. 1.3e-21;
Matches 58; Conservative 22; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.9%; Score 440.5; DB 7; Best Local Similarity 57.6%; Pred. No. 1e-35; Matches 83; Conservative 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RTDKSITQNS----NFLNINQQRG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-909-769-30; Sequence 30, Application US/10909769; Sequence 30, Application No. US20060024331A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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John Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VGCNDT-RYVGIRYFKVPDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                         APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal
FILE REFERENCE: 1581.0800001
CURRENT PILING DATE: 1090-11-05
PRIOR APPLICATION NUMBER: US/11-05
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                     DB 6; Length 849;
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                                                                                                Query Match
Best Local Similarity 57.6%; Pred. No. 7.4e-36;
Matches 83; Conservative 26; Mismatches 30; Indels
                              ; OTHER INFORMATION: Amino acid sequence of HC
US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 RIDKSITONS----NFLNINOORG 139
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DPNKYVDVNNVGIRGYMYLKGPRG 912
                                                                                                                                                                                                                                                                                                                                                                                              120 RIDKSITONS----NFLNINGORG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                              671 DPNKYVDVNNVGIRGYMYLKGPRG 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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            PEATURE:
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US/11/062
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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M
US/11/062,4711.7
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APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, John Mark
APPLICANT: SILMAN, Nigel
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal
CURRENT FILMS DATE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT APPLICATION NUMBER: 09/831,050
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
SOFTWARE: PATENT DATE: 1998-11-05
SOFTWARE: PATENT DATE: 1998-11-05
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                                                               Length 1070;
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                                                                                                                       Indels
                                                           DB 7;
                                               Query Match
37.4%; Score 284.5; DB 7
Best Local Similarity 39.3%; Pred. No. 2.6e-20;
Matches 59; Conservative 27; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                119 -----LRTDKSI-----TQNSNFLN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                         885 KNSYIKLKKDSPVGEILTRSKYNQNSKYIN 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/11062471A
Publication No. US20050255093A1
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Best Local Similarity 39.3%
Matches 59; Conservative
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                                                                                                                                                                                                                                                         APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei Jen
APPLICANT: Lin, Wei Jen
APPLICANT: Lin, Wei Jen
APPLICANT: Ackis Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REPERENCE: ALLEOUO (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTHARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker, US/11/062,471A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNL-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 GDVDRTQFIMMKYFSIFNTQLNGSNIKEIYKIGSYSEYLKDFWGNPLMYNKEYYMFNAGN 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/11062471A

| Publication No. US20050255093A1
| Publication No. US20050255093A1
| Publication No. US20050255093A1
| Publication No. US20050255093A1
| APPLICANT: SHONE, OILfford Charles
| APPLICANT: SUTTON, John Mark
| APPLICANT: HALLIS, Bassam
| APPLICANT: HALLIS, Bassam
| APPLICANT: HALLIS, Bassam
| APPLICANT: HALLIS, Bassam
| APPLICANT: SULMAN, NIGEL
| FILE REPRESENCE: 1591.0800001
| TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
| FILE REPRESENCE: 1591.0800001
| CURRENT APPLICATION NUMBER: 09/831,050
| PRIOR FILING DATE: 1999-11-05
| PRIOR FILING DATE: 1999-11-05
| PRIOR FILING DATE: 1999-11-05
| PRIOR FILING DATE: 1999-11-05
| PRIOR FILING DATE: 1999-11-05
| NUMBER OF SEQ ID NOS: 11
| SOFTHARE: PatentIn Ver. 2.1
| LENGTH: 1070
612 NCTDTTKFVWIKDFNIFGRELNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFN 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.9%; Score 296; DB 6; Length 900 39.9%; Pred. No. 1.6e-21; Live 29; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 -----LRTDKSI------TQNSNFLNINQQRGVY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNSYIKLVKDSSVGEILIRSKYNQNSNYIN---YRNLY 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-20
                                                                                                                                                                             Sequence 20, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 39.99
Matches 63; Conservative
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604 DENIDENQMLWIRDFNIFSKELSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDN 663
                                                                                                     61 -VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDBPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 NKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGC-NDTRYVGIRY
                                  1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 FKVFDTELGKTELETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%; Score 240.5; DB 7; 42.0%; Pred. No. 7.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT APPLICATION UNMER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PELLING DATE: 2003-03-11
PRIOR PELLING DATE: 2002-09-12
PRIOR PELING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR APPLICATION NUMBER: PCT/GB97/02273
PRIOR PILING DATE: 1997-08-22
PRIOR PLING DATE: 1997-08-22
PRIOR PLING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 141, Application US/11077550 Publication No. US20050244435A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quinn, Conrad Padraig
Foster, Keith Alan
Chaddock, John
Marks, Phillip
Sutton, J. Mark
Stancombe, Patrick
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                                                                                                                                                                                                           120 RTDKSITQNSNFLNING 136
                                                                                                                                                                                                                                                              664 YIDRYİAPESNVLVLVQ 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Clostridium tetani
US-11-077-550-141
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Best Local Similarity 42.0%
Matches 47; Conservative
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APPLICANT:
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APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REPERBYCE: ALLEGOID-100 (RO12003.146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCND-TRYVGIRYFKVPDTELGKTELETLYSDEPDPSILKDFWGNYLLYNKRYYLLNL-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PNYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.4%; Score 284.5; DB 7; Length 1169; Best Local Similarity 39.3%; Pred. No. 2.9e-20; Matches 59; Conservative 27; Mismatches 45; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 834;
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                                                                        APPLICANT: STANCOMB, PATICK
APPLICANT: STANCOMB, PATICK
APPLICANT: STANCOMB, PATICK
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR PILING DATE: 1990-02-23
PRIOR PILING DATE: 1990-02-23
PRIOR PILING DATE: 1990-02-23
PRIOR APPLICATION NUMBER: 08/785,829
PRIOR PILING DATE: 1990-02-23
PRIOR PILING DATE: 1996-12-27
PRIOR PELING DATE: 1996-12-37
PRIOR PILING DATE: 1996-12-13
PRIOR PELING DATE: 1996-12-13
PRIOR PELING DATE: 1996-10-13
PRIOR APPLICATION NUMBER: GB9625996.5
PRIOR PELING DATE: 1996-10-13
PRIOR PELING DATE: 1996-10-13
PRIOR PELING DATE: 1996-10-13
PRIOR PELING DATE: 1996-10-13
PRIOR PELING DATE: 1996-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 -----LRTDKSI------TQNSNFLN 133
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COTHER INFORMATION: Amino acid seqence of HC US-10-909-769-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10909769
Publication No. US20060024331A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Clostridium botulinum US-11-077-550-20
                                  Sutton, J. Mark
Stancombe, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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LENGTH: 834
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LENGTH: 11
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TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist FILE REFERENCE: ALLEO10-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
TYPE: PRT
ORGANISM: Artificial sequence
CRADISM: Artificial sequence
CRADISM: Artificial sequence of HC
US-10-909-769-22
                                                                                                                                                                                                                                                                                                           7
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31.4%; Score 239; DB 6; Length 842;
Best Local Similarity 37.0%; Pred. No. 6.3e-16;
Matches 54; Conservative 25; Mismatches 57; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 YYLLNLLRTDKSITQNSNFLNINQQR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||::|: | : : | | : | 63 YYMVNIDYLNRYMYANSRQIVFNTRR 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 2, 2006, 01:18:30 Job time : 6.84687 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on: March 2, 2006, 00:31:42 ; Search time 68.5139 Seconds (without alignments) 917.057 Million cell updates/sec

(Wichout alignments)
917.057 Million cell
18. TR.OR-081-087R-4

Title: US-08-981-087B-4
Perfect score: 757

Pertect score: 757 Sequence: 1 NIFSNTRLYTGVEVIIRKNG......TSSNGCFWSFISKEHGWQEN 143

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 2443163

2443163 segs, 439378781 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A\_Geneseq\_21:\*
1: geneseq\_21:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp2004s:\*
9: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Aaw68395 Clostridi Adz36069 C. botuli Adz36073 C. botuli Aav77144 Botulinum		Adz60276 BONT/A pr Aab04089 Botulism Aab04090 Botulism Aab04088 Botulism Aar95008 Type A ne		Aaw68390 Clostridi Ad269764 Botulinum Aay93307 A mangane Aay93310 A mangane
AAW68395 ADZ36069 ADZ36073 AAY77144	AAB3633 ADW24418 ADZ60271 AAB04083	ADZ60276 AAB04089 AAB04090 AAB04088 AAR95008	AAW68389 AAY77134 AAW68391 AAR95009	AAW68390 ADZ69764 AAY93307 AAY93310
451 2 74 9 73 9	382 382 382 382 415 415	425 433 433 434 438 244 438	438 2 438 3 445 2 462 2	462 2 859 9 1067 3
44 44 9.0 6.0 9.5 7.6 9.5 7.6 9.5	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	04 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	40.5 40.5 40.5 5	40.5 2.04 2.05 3.05
374.5 366 350.5	306.5 306.5 306.5 506.5	306.5 306.5 306.5 306.5	306.5 306.5 306.5 306.5	306.5 306.5 306.5 306.5
25 27 27 27	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	38 39 44 11	4 4 4 4 ሪ ሬ 4 ጊ

## ALIGNMENTS

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA;

WPI; 1997-065467/06.

Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.

Claim 5; Page 19; 37pp; English.

Novel polypeptides (AAM09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BONT/F). They lack the L chain and RN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine produce. Recombinant polypeptides can be produced in transformed host cells, as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 143 AA;

Query Match . 100

100.0%; Score 757; DB 2; Length 143;

120 408

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New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine against botulism.
61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                      349 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYXNNI
                                                                                                                                                                                                                                                                                                                    Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                      Botulism toxin heavy chain C-terminal sequence (serotype F).
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                                                                    121 RKNTSSNGCFWSFISKEHGWQEN
                                                                                     409 RKNTSSNGCFWSFISKEHGWQEN
                                                                                                                                                                                      AAB04103 standard; protein; 432
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99US-0133866P.
99US-0133867P.
99US-0133869P.
99US-0133869P.
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith LA, Byrne MP,
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N-PSDB; AAAS4499.
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12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
                                                                                                                                                                                                                                                         11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                            infection.
                                                                                                                                                                                                                                                                                                                           Botulism;
                                                                                                                                                                                                                         AAB04103;
                                                                                                                                                        RESULT 3
                                                                                                                                                                        AAB04103
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                                                                                                                                              61 KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLIGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278)
                                                                                                                         KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a type F botulinum neurcoxin (DNT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine produ. Recombinant prolypeptides can be produced in transformed host calls, sep. as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                         1 NIFSNIRLYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                        1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism.
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100.0%; Score 757; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic type F botulinum toxin heavy chain (aa848-1278).
                          IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasechnik VA;
                          ö
        Pred. No. 4.4e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum; type F strain Langeland
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minton NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                             RKNISSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                           RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 16-17; 37pp; English.
                                                                                                                                                                                                                                                                                                               AAW09014 standard; protein; 431 AA
                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-GB001409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95GB-00011909
          100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-065467/06.
N-PSDB; AAT48100.
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9641881-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1996;
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31-MAR-1997
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AAW09014;

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Best Local Matches 14

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Dotulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of a consisting of transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressed in a recombinant consisting and expressible in a recombinant consisting and expressible in a recombinant collection are advantageous since it eliminates the need recombinant nucleic acids are advantageous since it eliminates the need consistent of the contract of the consisting of the consisting bacterium.

The cost of production is lower. The nucleic acids can be derived from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived from the constant acids can be derived to the constant acids acids acids acids acids acids acids acids acids acids acids acids
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Best Local Similarity
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Clostridium botulinum serotypes A-G
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01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                      AAE07894;
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                                                                                                                                                                                                                                                                                                                                                         AAE07894
ID AAE(
                                                                                                                                                                                                                                                                                                                                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a carboxy-terminal linked by a carboxy-terminal (HN) bortion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant corpus and expressible in a recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producting bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                    350 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNI 409
                                                                                               61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
   ö
                                                                                                                                                                                                                                                                                                                                                                          Botulism toxin heavy chain C-terminal sequence (serotype F).
 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LA, Byrne MP, Middlebrook JL, Lapenotiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND
 0; Mismatches
                                                                                                                                                                                410 RKNTSSNGCFWSFISKEHGWQEN 432
                                                                                                                                                               RKNTSSNGCFWSFISKEHGWOEN 143
                                                                                                                                                                                                                                                                              AAB04096 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 9b; 73pp; English.
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99US-0133866P.
99US-0133867P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0133873P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2000; 2000WO-US012890.
                                                                                                                                                                                                                                                                                                                                             (first entry)
     Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-016048/02.
N-PSDB; AAA54490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against botulism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200067700-A2
                                                                                                                                                                                                                                                                                                                                             11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                             infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                             AAB04096;
                                                                                                                                                                                                                                            RESULT 4
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a gent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial neurotoxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                           ö
                                                                                                                                                                                                                                                                                         61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                       1 NIFSNITRLYTGVEVIIRKNGSTDISNITDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                 Gape
                                                                                                                 .
                                               Length 432;
                                                                                                              Indels
                                                     Score 757; DB 4;
Pred. No. 1.8e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified clostridial heavy chain fragment #1.
                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                       RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKNTSSNGCFWSFISKEHGWQEN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE07894 standard; protein; 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silman N;
                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2000; 2000WO-GB004644.
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07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                            Ouery Match
Best Local Similarity 100.0
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium botulinum.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514643/56.
Sequence 432 AA;
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Thu Mar

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61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
         The present sequence
                                                                                                                                                                                                                                                                                                         Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection, Prion disease, Alzheimer' disease, hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; translocation domain; HN domain; DipT; Hc; botulinum type F neurotoxin; binding domain; BONT/F.
and infection. They are also useful in gene therapy. The present seque is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain of botulinum neurotoxin type (BONT/F) with translocation domain of diphtheria neurotoxin. (Updated 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                       1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; therapy; inflammatory mediator; intracellular trafficking;
                                                                                                                                                                                   .,
                                                                                                                                           100.0%; Score 757; DB 4; Length 645; 100.0%; Pred. No. 3e-70; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DipT HN domain-BoNT/F-Hc fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 12; Page 57-60; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                         RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                  RKNTSSNGCFWSFISKEHGWOEN 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE35692 standard; protein; 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                             Best Local Similarity .... Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-167247/16.
                                                                                                            Sequence 645 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE35692;
                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                           Query Match
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infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for inhibiting secretion from cells. The invention is also useful for increating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as obsphorospasm, torticolis and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct domprishing Corymebacterium diphtheriae diphtheria toxin translocation domprishin and botulinum type F neurotoxin from Clostridium botulinum. This sequence is used in the exemplification of the invention. (Updated on 23-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; CODD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONI/F; translocation domain; HN domain; DipT; Hc; binding domain;
                                                                                                                                                                                                                                                                                                                                                                                             1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                                  KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                               Gaps
     intracellular
                                                                                                                                                                                                                                                                                                                                                             ,
0
                                                                                                                                                                                                                                                                                                                        6; Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BoNT/F-Hc-DipT HN domain-thrombin linker fusion construct.
     treating
                                                                                                                                                                                                                                                                                                                  100.0%; Score 757; DB 6; 1
100.0%; Pred. No. 3e-70;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKNTSSNGCFWSFISKEHGWQEN 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKNTSSNGCFWSFISKEHGWOEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE35693 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium diphtheriae.
Clostridium botulinum.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       botulinum type F neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                        Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                 Sequence 645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200296467-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                      Query Match
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(MICR-) MICROBIOLOGICAL RES AUTHORITY.

WPI; 2003-167247/16.

Sutton JM,

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, toritolis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain), botulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
                        Example 12; Page 60-63; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                     KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                      9
                                                                                         515 NIFSNITKLYTGVEVIIRKNGSTDISNITDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                  1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                   Gaps
                                    ò
Query Match 100.0%; Score 757; DB 6; Length 657; Best Local Similarity 100.0%; Pred. No. 3.1e-70; Matches 143; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                         121 RKNTSSNGCFWSFISKEHGWOEN 143
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AAE35694 standard; protein; 657 AA. 17-JUN-2003 (first entry) AAE35694; **AAE3569**4 

BoNT/F-Hc-DipT HN domain-factor Xa linker fusion construct.

infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spaem; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/P; translocation domain; HN domain; DipT; Hc; binding domain; Apoptosis; therapy; inflammatory mediator; intracellular trafficking; botulinum type F neurotoxin

Corynebacterium diphtheriae. Clostridium botulinum. Unidentified. WO200296467-A2 05-DEC-2002 Chimeric

21-MAY-2002; 2002WO-GB002384

24-MAY-2001; 2001GB-00012687

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for medulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders incommend and account as blephorospasm, toritionis and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheriat toxin translocation domain (DipT-HW domain). botulinum type F neurotoxin binding domain (BONT/F-HC) from Closeridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. Example 12; Page 63-65; 130pp; English Sequence 657 AA; 

; 0 100.0%; Score 757; DB 6; Length 657; 100.0%; Pred. No. 3.1e-70; 0; Mismatches Query Match Best Local Similarity 100. Matches 143; Conservative

574 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120 9 1 NIPSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 61 셤 В ઠે ò

ઠ 셤 AAE07893 standard; protein; 685 AA 01-NOV-2001 (first entry) AAE07893;

RESULT 9

Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; botulinum neurotoxin type F; BONT/F. Modified clostridial heavy chain-superoxide dismutase conjugate #5

Geobacillus stearothermophilus Influenza virus. Clostridium botulinum. Synthetic Chimeric. 

WO200158936-A2

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for the invention are CC substances to neuronal cells. They are useful in gene therapy. The present sequence and infection. They are also useful in gene therapy. The present sequence and infection. They are also useful in gene therapy. The present sequence conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from C conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from C subsidial searchermophilus, linker that can be cleaved by factor Xa, translocation peptide from influenza virus and a neuronal cell-specific condiguate.
                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                           (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 43; 50pp; English.
                                                                                                                                                                                                                             Silman N;
                                                             04-DEC-2000; 2000WO-GB004644.
                                                                                                               02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                           Sutton JM,
                                                                                                                                                                                                                                                                     WPI; 2001-514643/56.
                                                                                                           02-DEC-1999;
                   16-AUG-2001
                                                                                                                                                                                                                           Shone CC,
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KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLIGFHSNNLVASSWYYNNI 662 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE Gaps 0 Length 685; 0; Indels 100.0%; Score 757; DB 4; 100.0%; Pred. No. 3.3e-70; ive 0; Mismatches 0; RKNTSSNGCFWSFISKEHGWQEN 143 Best Local Similarity 100. Matches 143; Conservative Query Match 61 603 121 ð g ઠે 셤 ð

Sequence 685 AA;

RKNISSNGCFWSFISKEHGWQEN 685

663

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Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F. Modified clostridial heavy chain-superoxide dismutase conjugate #2. AAE07890 standard; protein; 862 AA. (first entry) 01-NOV-2001 AAE07890; 

The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CS including neurodespenarative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence conjudic constructs as as a sectival and mn-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase conjugate. This conjugate comprises bacterial hn-superoxide dismutase conjugate. This conjugate comprises bacterial in gene that can be cleaved by factor xa, translocation domain from diphtheria neurotoxin and a neuronal cell. New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells. (MICR-) MICROBIOLOGICAL RES AUTHORITY. Example 9; Page 40; 50pp; English Silman N; Geobacillus stearothermophilus. 02-DEC-1999; 99GB-00028530. 07-APR-2000; 2000GB-00008658. 04-DEC-2000; 2000WO-GB004644 Corynebacterium diphtheriae. Clostridium botulinum. Shone CC, Sutton JM, WPI; 2001-514643/56. Sequence 862 AA; WO200158936-A2 16-AUG-2001 Synthetic Chimeric. 

780 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLIGFHSNNLVASSWYYNNI 61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 121 RKNTSSNGCFWSFISKEHGWOEN 143 840 RKNTSSNGCFWSFISKEHGWQEN 862 AAE07892 standard; protein; 887 AA. 01-NOV-2001 (first entry) AAE07892; RESULT 11
AAE07892
ID AAE07.
XX
AC AAE07.
XXX
DT 01-NO' 셤 g 요 ò ઠે

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0; Gaps

0; Indels

100.0%; Score 757; DB 4; 100.0%; Pred. No. 4.4e-70; ive 0; Mismatches 0;

143; Conservative

Query Match Best Local Similarity

Best Loca Matches

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1 NIFSNIRLYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE

779

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AAE35713 standard; protein; 979

RESULT 12

AAE35713

17-JUN-2003 (first entry)

AAE35713;

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (arboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino et aminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocates the therapeutic agent into the neuronal cell, where the translocates the therapeutic at M domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to reat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase (mNSOD), MNSOD from Bacillus stearotheramophilus, linker that can be cleaved by thrombin, translocation domain from chiptheria neurotoxin and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         745 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 804
                                  Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
  clostridial heavy chain-superoxide dismutase conjugate #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 757; DB 4;
100.0%; Pred. No. 4.6e-70;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 42; 50pp; English.
                                                                                                                                     Homo sapiens.
Geobacilus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                     04-DEC-2000; 2000WO-GB004644
                                                                                                                                                                                                                                                                                                                                                                                            99GB-00028530.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514643/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 887 AA;
                                                                                                                                                                                                                                                                        WO200158936-A2
                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1999;
                                                                                                                                                                                                                                                                                                             16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shone CC,
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                                                                                                                                                                                                                                    Chimeric
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Matches
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(COPD), bronchitis and aschma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HN domain), botulinum type F neurotoxin binding domain (BoNT/F-HO from Clostridium botulinum and factor Xa linker peptide and Yersinia pestis targeted effector protien YopT. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for mediating expression of cell-surface markers and for trafficking, for mediating expression of cell-surface markers and for trafficking, for mediating expression of cell-surface markers and for
                                                                            BoNT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypersecretion disorders such as chronic obstructive pulmonary disease
                                                                                                                       Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; HC; binding domain; botulinum type F neurotoxin; targetted effector protien; YopT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Page 110-114; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001GB-00012687
                                                                                                                                                                                                                                                                                            Corynebacterium diphtheriae. Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shone CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-167247/16.
                                                                                                                                                                                                                                                                                                                                            Yersinia pestis.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 979 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200296467-A2.
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Length 979; Indels

100.0%; Score 757; DB 6; 100.0%; Pred. No. 5.2e-70; iive 0; Mismatches 0;

Matches 143; Conservative Query Match Best Local Similarity

> 865 RKCNTSSNGCFWSFISKEHGWQEN 887 RKNTSSNGCFWSFISKEHGWQEN 143

121

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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60

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The invention relates to a non toxic polypeptide, for delivery of a the invention relates to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a gagnification in the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for teat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence continuence to neuronal in gene therapy. The present sequence continuence to the continuence to the continuence to the continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence continuence
New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
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                                                                                                           KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum C2 translocation domain with BoNT/F-binding domain #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                     RKNTSSNGCFWSFISKEHGWQEN 979
                                                                                                                                                                                      RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                 AAE07901 standard; protein; 1032 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514643/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                                                neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                 Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell;
                                                                                                                                                                                                                                                                                                                                A manganese superoxide dismutase (Mn-SOD) construct.
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100.0%; Pred. No. 5.7e-70;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shone CC, Sutton JM, Hallis B, Silman N;
                                                                                                                                  1010 RKNTSSNGCFWSFISKEHGWQEN 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 48-51; 65pp; English.
                                                                                                                   143
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                                                                                                                 RKNTSSNGCFWSFISKEHGWQEN
                                                                                                                                                                                                                              AAY93309 standard; protein; 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geobacillus stearothermophilus.
Clostridium botulinum.
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Best Local Similarity 100. Matches 143; Conservative

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NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE

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                                  The present sequence represents a construct of the invention, comprising a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SOD). A Bacillus stearothermophilus Mn-SOD, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and
                61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                                                                                                                                                                                                                                                                                                            Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
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                                                                                                                                                                                                                                                                                                               A manganese superoxide dismutase (Mn-SOD) construct
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100.0%; Score 757; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hallis B, Silman N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                          1037 RKNTSSNGCFWSFISKEHGWQEN 1059
                                                                                    121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                            AAY93312 standard; protein; 1084 AA.
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Geobacillus stearothermophilus.
Clostridium botulinum.
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942 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 1001
                                                                                                             KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                    2, 2006, 00:38:56
                                                                                                                                                                                                                                    1062 RKNTSSNGCFWSFISKEHGWQEN 1084
                                                                                                                                                                                       121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                               Search completed: March
Job time: 68.5139 secs
             917 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 976
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein search, using sw model OM protein

2, 2006, 00:39:17 March Run on:

; Search time 11.9443 Seconds
(without alignments)
1151.928 Million cell updates/sec

1 NIFSNTRLYTGVEVIIRKNG.......TSSNGCFWSFISKEHGWQEN 143 US-08-981-087B-4 757 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

PIR 80:\*
1: pir1:\*
3: pir2:\*
5: pir3:\*
: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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1	Description	neurotoxin type F	botulinum neurotox	botulinum neurotox	botulinum neurotox	bontoxilysin (EC 3	botulinum neurotox	::	bontoxilysin (EC 3	neurotoxin - Clost	tentoxilysin (EC 3	probable protein-h	type E neurotoxin	botulinum neurotox	UV-damaged DNA bin	asparagine-rich pr	envelope polyprote	hypothetical prote		hypothetical prote	Ω.	surface-layer rela	ď	trfA protein - sli	asparagine-rich pr		hypothetical prote		asparagine-rich bl	asparagine-rich pr
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;	OI .	140813	S33411	S21178	JH0256	BTCLAB	I40645	140631	A48940	S39791	BICLIN	T09057	A53878	S11455	S71092	S14577	860538	S73786	T08605	A64474	H64130	D97142	E97302	T14004	S14556	T18420	D71612 ·	B71704	C45600	A23770
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	Match	80.2	8.94	3.0	9.5	0.5	4.6	۲.1	9.7	8.8	8.1	4.3	4.2	3.7	5.9	2.7	2.5	2.1	5.0	5.0	1.7	1.7	11.7	1.6	1.6	1.4	11.4	1.4	1.3	J.3
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16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C;Accession: 140813; S48108
R;Bast, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.E R;Bast, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.E FEMS Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum. A;Reference number: I40644
A;Accession: I40813

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-1274 «RES>
A;Residues: 1-1274 «RES>
A;Residues: 1-1274 «RES>
A;Cross-references: UNIPROT: B30996; UNIPARC: UPI0000126B8A; GB:M92906; NID:g144866; PIDN:
A;Ccampbell, K.D.; Colling, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
J. Title: Gene probbes for identification of the botulinal neurotoxin gene and specific id
A;Reference number: \$48103; MUID:94013372; PMID:8408542
A;Accession: \$48108

Status: preliminary; translation not shown

A, Molecule type: DNA A, Residues: 634-1002 < CAM>

A; Cross-references: UNIPARC: UP1000016EA7B; EMBL:X70816; NID:g407788; PIDN:CAAS0147.1; PIC; Superfamily: tetanus toxin C; Keywords: neurotoxin

ö Gaps 4; Length 1274; Score 607; DB 2; Length 12 Pred. No. 1.9e-45; 8; Mismatches 12; Indels Query Match
Best Local Similarity 83.1%;
Matches 118; Conservative

9 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE à g

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RKNTSSNGCFWSFISKEHGWQE 142 1253 121 ð 유

# RESULT

botulinum neurotoxin type F - Clostridium barati C;Species: Clostridium barati C;Date: 13.-Jan-1995 #sequence\_revision 13.-Jan-1995 #text\_change 09.Jul-2004 C;Accession: 833411; 831860 R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T PEMS Microbiol. Lett. 108, 175-182, 1993

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A;Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin A;Reference number: 833411; MUID:93252228; PMID:8486245
A;Accession: 833411
A;Accession: 833411
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1268 <TMO>
A;Residues: 1-1268 <TMO>
C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1187 KTIKLRRISNSNYNSNQMIIMDSIGDNCTWNFKTNNGNDIGLLGFHLNNLVASSWYYKNI 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                         Length 1268;
                                                                                                                                                                                                                                                                                                      76.8%; Score 581; DB 2; Length 12 76.8%; Pred. No. 3.7e-43; ive 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1247 RNNTRNNGCFWSFISKEHGWQE 1268
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Biochimie 72, 213-217, 1990
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                              Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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Best Local
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A; Molecule type: protein

A; Residues: 420-427 < Calm.
A; Residues: 420-427 < Calm.
A; Cross-references: UNIPARC: UPI0000176710

A; Experimental source: strain Beluga
A; Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin C; Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit ne C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RiPoulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
abothem. Bloghyea Res. Commun. 183, 107-113, 1992
A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum typ.
A;Reference number: JH0256; MUID:92181428; PMID:1543481
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A;Residues: 1-27, E', 29-1251 <POU>
A;Cross-references: UNIPMCT:P30955; UNIPARC:UPI000017670D; EMBL:X62088; NID:g40379
A;Cross-references: University A;Cross-references: Unipartial Ance 43755
B;Pujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N
Cgn. Microbiol. 137, 519-525, 1991
A;Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E tox
A;Reference number: S16145; MUID:91237316; PMID:2033376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain BL6340
C, Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release
C, Comment: The heavy chain mediates the binding of toxin to cell receptors while the li
A:Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the A;Reference number: A60027; MUID:90344918; PMID:2116911
A;Accession: A60027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-422/Product: botulinum neurotoxin type E light chain #status predicted <LCH>F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>F;412-426/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        botulinum neurotoxin type E precursor - Clostridium butyricum
C;Species: Clostridium butyricum
C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 RLYTGVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.5%; Score 374.5; DB 2
54.7%; Pred. No. 5.8e-25;
iive 24; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: JH0256
A;Status: nucleic acid sequence not shown
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A; Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C; Superfamily: tetanus toxin C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot E; 244, Product: bontoxilysin A light chain #status experimental <LGHT> F; 445-1256, Product: bontoxilysin A heavy chain #status experimental <HVY> F; 223, 227/ Binding site: zinc (His) #status predicted F; 224/Active site: Glu #status predicted
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Cross-references: UNIPROT:Q45894; UNIPARC:UP1000016EA88; EMBL:X73423; NID:g507070; PIC
                                                                                                                                                                                                                                                                                                                                                    Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum type
                                                                                                                                                                                    E.; Suedhof, T.C.; Jahn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum neurotoxin type A - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40645 A.K.; Lawson, P.A.; Collins, M.D.
Rs: Willems, A.; Bast, A.K.; Lawson, P.A.; Collins, M.D.
A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botul
A;Reference number: I40645; MUID:94143603; PMID:8310180
Partial sequence of the light chain of botulinum neurotoxin type A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV
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                                                                                                                                                  A,Cross-references: UNIPARC:UP10000173659
R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, D. Biol. Chem. 269. I617-1620, 1994
A;Title: Proteclysis of SNAP-25 by types E and A botulinal neurotoxins. A;Reference number: A49708; MUID:94124495; PMID:8294407
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Pred. No. 3e-18;
2; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
40.5%; Score 306.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 6e-19;
Matches 67; Conservative 21; Mismatches 50;
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43.4%; Pre-
tive 22;
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                                                                                                Molecule type: protein: Residues: 2-47 <DAS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 66; Conserv
                                                                                                                                                                                                                                                                                                                         ;Contents: annotation
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                                                                  Accession: A27000
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Matches
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A; Residues: 1-1256 <BIN>
A; Residues: 1-1256 <BIN>
A; Experimental source: strain 62A, subtype A
B; Experimental source: strain 62A, subtype A
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
Bur. J. Blochem. 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin
A; Reference number: S09492; MUID: 90235864; PMID: 2185020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross-references: UNIPARC:UPI0000173655, EMBL:D67030; DDBJ:D50421; NID:g2160224; Betley, M.J.; Somers, E.; DasGupta, B.R. iochem. Biophys. Res. Commun. 162, 1388-1395, 1989; Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term Reference number: A33401; MUID:89350959; PMID:2669749
                                                                                                                                                                                                                                                                                                                                                                                                                    N'Alternate names: botulinum neurotoxin type A
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Al-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other A;Reference number: A35294; WuID:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1, 0, 3-26, VV, 28-1296 <THO>
Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: NCTC 2916
FF Ujita, R.; Fujitanga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A; Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A; Reference number: 867988; MUD: 96096783; PMID: 8521962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-35 <BET>
Cross-references: VINPARC:UPI000016EA84; GB:M27892; NID:g144880; PIDN:AAA23269.1; PID:
Gimenez, J.A.; DasGupta, B.R.
Protein Chem. 12, 351-363, 1993
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Blochlimie 72, 661-664, 1990
A; Rille: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and ar A; Reference number: A60025; MUID:91120847; PMID:2126206
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                                                                                KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 867-880;1148-1217,'Y',1219 <GIM>
Cross-references: UNIPARC:UP100000BBB24; UNIPARC:UP10000173656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 2-6;445-453, XY,455-457 <DAS1>
A; Cross-references: UNIPARC:UP10000173657; UNIPARC:UP10000173658
R; DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1997
                                                                                                                                                                                                                                                                                                                                                                                                bontoxilysin (EC 3.4.24.69) A precursor - Clostridium botulinum
                                                                                                                                                                                                           |:||| ||:|||||
1232 TNSNGFFWNFISEEHGWQE 1250
                                                                                                                                                                   124 TSSNGCFWSFISKEHGWQE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S09492
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A;Status: nucleic acid sequence not shown
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A; Residues: 1-313,'S',315-451 <KUR>
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 2-17 < SCH2>
A; Cross references: UNIPAR
A; Accession: 508574
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Molecule type: protein
Residues: 2-16 <SCH1>
preliminary
                                                                                                                                                                       C)Date: 12-Nug-1996 ##sequence revision 12-Aug-1996 #text_change 09-Jul-2004
CAccession: 140631; S48103; $48104; $36015
R;Hutson, R.A.; Colling, M.D.; Batt, A.K.; Thompson, D.E.
Curr. Microbiol. 28, 101-110, 1994
A;Title: Nucleoride sequence of the gene coding for non-proteolytic Clostridium botulinu
A;Reference number: 140631; MUID:94122659; PMID:7764370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1291 ARBS>
A; Residues: 1-1291 ARBS>
A; Residues: 1-1291 ARBS>
A; Cross=references: UNIPROT: Q08077; UNIPARC: UPI00000BDC86; EMBL: X71343; NID: g296148; PID R; Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A; Reference number: $48103; MUID: 94013372; PMID: 8408542
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MARCOLINE (EC 3.4.24.69) B precursor - Clostridium botulinum
NiAlternate names: botulinum neurotoxin type B (BoNT/B)
Species: Clostridium botulinum
C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48940; S48105; S21575; A42871; S0155; S08562; S07128; S08574
FWhelan, S.M.; Blmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Brviron. Microbiol. S8, 2345-2334, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the typ
A;Reference number: A48940; MUID:92384550; PMID:11514783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 634-497, 'Y', 845,'N', 847-994 <CAM2>
A; Residues: 634-843,'T', 845,'N', 847-994 <CAM2>
A; Cross-references: UNIPARC: UPI0000097A6E; EMBL: X70819; NID: 9407780; PIDN: CAA50150.1; E
A; Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)
C; Comment: Botulinum neurotoxin type B in these strains may posses a capable catalytic
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 634-761, E',763-841, M',843, T',845, N',847-994 <CAMI>
A;Cross-references: UNIPARC:UPIO000018AEF; EMBI:X70814; NID:9407778; PIDN:CAAS0145.1; A;Experimental source: non-proteolytic strain 21298 (Scott)
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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(Superfamily: tetanus toxin
(Staywords metalloprotein; neurotoxin; transmembrane protein; zinc
(1244/Product: botulinum neurotoxin type B light chain #status predicted <LGHT>
(1442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVY>
(1230,234/Binding site: zinc (His) #status predicted
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21.1%; Score 160; DB 2;
Best Local Similarity 29.2%; Pred. No. 4.8e-06;
Matches 47; Conservative 28; Mismatches 66,
                                                                                                                                                                                                                                                                                                                                                                                                            Accession: 140631
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
                                                                                                                                                Species: Clostridium botulinum
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PID
A; Residues: 1-1291 (MHE)
A; Cross-references: UNIPROT: P10844; UNIPARC: UP1000016EA76; GB: M81186; NID: g144734; PIDN
A; Cross-references: UNIPROT: P10844; UNIPARC: UP1000016EA76; GB: M81186; NID: g144734; PIDN
A; Experimental source: type B, Danish
A; More: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this public
R; Campbell, K.D.; Collins, M.D.; East, A.K.
A; Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene and specific is A; Reference number: S48103; MUID:94013372; PMID:8408542
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A;Accession: breliminary
A;Astatus: preliminary
A;Actatus: protein
A;Residues: 442-459 < SCH3>
A;Cross-references: UNIPARC:UP10000173652
B;Across-references: UNIPARC:UP10000173652
B;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.
Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the light chains of tetanus to
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C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaps
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: UNIPARC:UP10000013742
A.Experimental source: strain Okra
A.Note: sequence extracted from NCBI backbone (NCBIP:109365)
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
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B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
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B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
B.Dascupta, B.R.: Datta, A.
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A.Molecule type: DNA
A.Roclestions: S21575
A.Molecule type: DNA
A.Roclestides: 36-217, 07, 219-224, 08, 0226-246 (SZA>
A.Roclestides: 36-217, 07, 219-224, 08, 020016EA79; EMBL: 211934; NID: 940383; PIDN: CAA77991.1; PI
R.Kurazono, H.; Mochida, S.; Binz, T.; Bisel, U.; Quanz, M.; Grebenstein, O.; Wernars, J. Biol. Chem. 267, 14721-14729, 1992
A.Title: Minimal essential domains specifying toxicity of the light chains of tetanus the A.Reference number: A42871; MUID: 92340509; PMID: 1634516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Status: preliminary
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 634-994 CCAM>
A/Residues: 634-994 CCAM>
A/Residues: 634-994 CCAM>
A/Residues: 614-994 CCAM>
A/Residues: 614-994 CCAM>
A/Reperimental source: proteolytic type B, strain NTC 7273
A/Residue E.A.; Pemberton, J.M.; Desmarchelier, P.M.
R/Szabo, E.A.; Pemberton J.M.; Desmarchelier, P.M.
A/Bescription: Partial amino acid sequence of botulinum neurotoxin type B and comparis
A/Reference number: 821575
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A; Molecule type: protein
A; Residues: 2-29, 'M',31-45 < DAS>
A; Cross-references: UNIPARC:UP10000173650
A; Accession: S08562
A; Molecule type: protein
A; Residues: 442-463, 'R',465-467 < DA2>
A; Cross-references: UNIPARC:UP10000173650
B; Schmidt, J.J.; Sathyamoorthy, V; DasGupta, B.R.
Arch. Biochim. Biophys. 238, 544-548, 1985
A; Title: Partial amino acid sequences of botulinum neurotoxins type
A; Reference number: 807128; MUID:85197963; PMID:3888113
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;Molecule type: DNA
;Residues: 1-1315 <EIS>
;Cross-references: UNIPROT:P04958; UNIPARC:UP100003617E; GB:X04436; NID:g40769; PIDN:C.
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; Molecule type: DNA
; Residues: 1-1315 - CRA1>
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;Cross-references: UNIPARC:UP10000156CFA; GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:
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,Title: Isolation, purification, and characterization of fra;Reference number: A60759; MUID:90035436; PMID:2478476
                                                                                                                    ;Fairweather, N.F.; Lyness, V.A.
Uncleic Acids Res. 14, 7809-7812, 1986
Yfitle: The complete uncleotide sequence of tetanus toxin.
yReference number: A25757; MUID:87040747; PMID:3774547
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Residues: 865-894 <FA3>
Cross-references: UNIPARC:UP1000017364D
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A;Residues: 461-475 <MAT>
A;Cross-references: UNIPARC:UP1000017364E
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A,Reference number: A25689; MUID:87053814; PMID:3536478
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neurocoxin - Clostridium botulinum
C;Species Clostridium botulinum
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C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
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N;Alternate names: tetanus neurotoxin
C;Species: Clostridium tetani
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A25689; A25757; Ā25194; B25194; A60759; S69348; S09364
R;Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, EMBO J. 5, 2495-2502, 1986
C. Function:
A; Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
A; Description: catalyzes toxin
C; Superfamily: tetranus toxin
C; Superfamily: tetranus toxin
C; Superfamily: tetranus toxin
P; 2-441/Product: bontoxilysin B light chain #status experimental <LGHT>
P; 2-441/Product: bontoxilysin B heavy chain #status experimental <HVY>
P; 230, 234/Binding site: zinc (His) #status predicted
P; 231/Active site: Glu #status predicted
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J. Immunol. 142, 394-402, 1989
A.Title: Delineation of several DR-restricted tetamus toxin T cell epitopes.
A.Fatile: Delineation of several DR-restricted tetamus toxin T cell epitopes.
A.Reference number: J85098; MUID: 8903918; PMID: 2463305
A.Contents: annotation; epitope region
R.Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R. Nature 359, 832-835, 1992
A.Title: Tetamus and botulinum-B neurotoxins block neurotransmitter release by proteolyt A.Reference number: S27125; MUID: 93063293; PMID: 1331807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Comment: The source of this protein was an extrachromosomal plasmid.
C.Comment: The source of this protein was an extrachromosomal plasmid.
C.Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C.Comment: Fragment B forms ion channels in a lipid blayer. Fragment C binds to ganglio C.Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
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F; 234/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ride Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C. Eur. J. Blochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin A;Reference number: S69348; MUID:95262688; PMID:7744050
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52;

IndelB

	QY         7 RLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKII 63           Db         66 RLYSGIKVKIQRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKKI 121           Qy         64 K 64           Db         122 K 122
SULT 11 3057 Dable prote Dable prote Dable prote Caterine na Sucession: Tingleton, C Sucession: Tratus: prel Colorule typ	RESULT 13 51455 botulinum neurotoxin type D - Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Accession: S11455 R;Silar, T; Kurazono, Kurazono, Kurazono, Kurazono, Kurazono, Kurazono, Kurazono, S11455 Nuclesion: S11455 A;Nocession: S11455 A;Nocession: S11455 A;Steue: perplainiary; translation not shown A;Nolecule type: DNA A;Nolecule typ
RESULT 12 A53878 LYPE E neurotoxin - Clostridium botulinum (fragments) C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Species:	RESULT 14 Sy1092 UV-damaged DNA binding protein repE - slime mold (Dictyostelium discoideum) C;Species: Dictyostelium discoideum C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 R;Adexander, H.; Lee, S.K.; Yu, S.L.; Alexander, S. R;Alexander, H.; Lee, S.K.; Yu, S.L.; Alexander, S. Nucleic Acids Res. 24, 2295-2301, 1996 A;Title: repE-The Dictyostelium homolog of the human xeroderma pigmentosum group E gene i A;Reference number: S71092; MUD:96279729; PMID:8710499 A;Accession: S71092 A;Accession: S71092 A;Accession: S71092 A;Accession: S1092 A;Accession: S1092 A;Accession: S21443 A;Reference number: S1443 A;Reference number: S1443 A;Residues: B60-1139 <syd> A;Residues: B60-1139 <syd> A;Residues: B60-1139 <syd> A;Residues: B60-1139 <syd> A;Genetics: A;Accession: S21443 A;Residues: B60-1139 <syd> A;Genetics: A;Accession: S21443 A;Residues: B60-1139 <syd> A;Genetics: A;Accession: S21443 A;Residues: B60-1139 <syd> A;Genetics: TepE</syd></syd></syd></syd></syd></syd></syd>

C; Superfamily: UV-damaged DNA-binding protein

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A;Accession: S14577
A;Status: preliminary
A;Molecule type: mRNA
A;Redues: 1-391 <5GH>
A;Cross-references: UNIPROT:Q25768; UNIPARC:UPI000080C7F; EMBL:X17483; NID:g9842; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       apparagine-rich protein (clone 14Cl) - malaria parasite (Plasmodium falciparum) C.Species: Plasmodium falciparum C.Species: 20-Reb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                             66 IRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNN---IR 121
                                                                                                                                                                                                                           1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                            50 YEKKEIITKASGNAE----DTIGRPTEAGQLGIIDPDGRIVALHLY------EGLLKL 97
                                                                                                 9 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRD---VEYRLYADISIAKPEKIIKL
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; Pred. No. 0.47;
33; Mismatches 55; Indels 17; Gaps
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12.9%; Score 98; DB 2; Length 1139; llarity 28.0%; Pred. No. 1.2; Conservative 21; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S14577 _ _ _ _ Mueller-Hill, D. Schreiber, L.; Deutsche, U.; Storck, T.; Mueller-Hill, D. bmitted to the EMBL Data Library, December 1989; Reference number: S14469
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159 TTTTNNNNNNNNNN 174
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Best Local Similarity 22.8%;
Matches 31; Conservative 3
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Best Local Similarity
Matches 35; Conserv
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149 KNVNN 153
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 29, Last annotation update)
BONT/F (Neurotoxin type F).
Name=bont/f; Synonyms=bonT/F;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridium.
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Submitted (AUG-1994) to the EMBL/GenBark/DDBJ databases.
EMBL; X81714; CAA57358.1; -; Genomic_DNA.
EMBL; L35496; AAA23210.1; -; Genomic_DNA.
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
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HSSP, Q45894, 1E1H.

MEROPS, M27.002, ...

GO, GO:001621; C:integral to membrane; IEA.

GO, GO:001621; F:metallopeptidase activity; IEA.

GO, GO:0008237; F:metallopeptidase activity; IEA.

GO, GO:0008405; P:pathogenesis; IEA.

GO, GO:000508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR010591; Boculinum.

InterPro; IPR010595; Peptidase M27.

InterPro; IPR006025; Peptidase M27.

InterPro; IPR006025; Peptidase M27.

PRINTS; PR00760; BONTOXIINSIN;
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100.0%; Pred. No. 7.2e-58;
ive 0; Mismatches 0;
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Neurotoxin.
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                                                  097239_PLAF7
Q6TAN6_9HIV1
BXD_CLÖBO
Q9U0J0_PLAF7
Q81EH4_PLAF7
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PLAF7
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Q4Y9B4_PLABE
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                                 Q7RB38
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Q57236; Q45863;
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Best Local Similarity
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NCBI_TaxID=1491;
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(c) 1993 - 2006 Biocceleration Ltd.
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Q8XZM3 CLOBU
Q9YAR6 CLOBU
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Listing first 45 summaries
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Result No.

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                                                                                                                                                                                                                                                         MEDLINE=98440323; PubMed=9767710; DOI=10.1007/s002849900384; Santos-Buelga J., Collins M.D., East A.K.; "Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B & E
                                                                                                                                        Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BoNT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1280;
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; Pred. No. 1.9e-47;
10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SEQUENCE 1280 AA; 147486 MW; D0F748976EBC222C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Santos-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13631; CAA73972.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS, M27.002; -.. GO GO:0016021; C:integral to membrane; IEA. GO; GO:0008237; F:metallopeptidase activity; IEA. GO; GO:0008405; F:metallopeptidase activity; IEA. GO; GO:0006405; F:metallopeptidase activity; IEA. GO; GO:0006508; F:proteolysis and peptidolysis; IEA. InterPro; IPR01591; Botulinum. InterPro; IPR006025; Peptidase M27. InterPro; IPR006025; Pept M Zn BS. Fam; PP01742; Peptidase M27; I. PRINTS; PR00760; BONTOXITYSIN.
                                                               Created)
Last sequence update)
Last annotation update)
                                   1280 AA
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                                   PRT;
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                                                                                                                                                                                                                                                                                                                                           Curr. Microbiol. 37:312-318(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.4%;
84.5%;
                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAK-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.5%;
Matches 120; Conservative
                              Q9ZAJS_CLOBO PRELIMINARY;
Q9ZAJS;
                                                           01-MAY-1999 (TrEMBLrel.
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STRAIN=CDC 3281;
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                                                                                                                BonT protein.
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P30996;
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NEAUTHILIDATION OF SUBSTRATE.

RA MEDLINE=9423052; PubMed=8175689;
Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F.,
RA Reques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;
Roulinal neurocoxins and tetanus toxin.";
Corlinal neurocoxins and tetanus toxin.";
J. Biol. Chem. 269:1276-12772[194].

J. Biol. Chem. 269:1276-12772[194].

J. Biol. Chem. 269:1276-12772[194].

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J. Biol. Chem. 269:1276-12772[194].

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  East A.K., Collins M.D., "Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteclytic Clostridium botulinum type F.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94013372; PubMed=8408542; Cambbell K.D., Collins M.D., East A.K.; Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                   East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A., Thompson D.E.;
                                                                                                                                                                                                                 STRAIN=Type F / ATCC 23387;
MEDLINE=93012902; Pubmed=1398040; DOI=10.1016/0378-1097(92)90408-G;
                                                                              Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                     "Sequence of the gene encoding type F neurotoxin of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M92906; AAA23263.1; -; Genomic DNA.
EMBL; S73676; AAC60475.1; -; Genomic DNA.
EMBL; X70820; CAA50151.1; -; Genomic DNA.
EMBL; X70816; CAA50147.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                             FEMS Microbiol. Lett. 75:225-230(1992).
  Botulinum neurotoxin F heavy chain]
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MEDLINE=94297488; PubMed=7764998;
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STRAIN=Type F / Hobbs FT10;
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STRAIN=Type F / ATCC 23387;
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                                                     Clostridium botulinum.
                                                                                                                                   NCBI TaxID=1491;
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PIR, 140813; 140813. PIR, S48109; S48109. HSSP; Q45894; 1E1H. MEROPS; M27.002; -.

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ProDom; PD001963; Botulinum; 1. PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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                               Neurotoxin.
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EMBL; X68262; CAA48329.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                   1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
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                                                                                                                                                                              1 436

437 1274

Botulinum neurotoxin F light chain.
228 228 8 pimilarity.
227 227 220 220 Catalytic (By similarity).
231 231 Zinc (catalytic) (By similarity).
429 445 Interchain (between light and heavy chains) (Probable).

1274 AA; 146710 MW; 5899756A7438B921 CRC64;
             InterPro; IRR066025; Pept M Zn BS.
InterPro; IRR006025; Pept M Zn BS.
InterPro; IRR0019928; Toxin_recpt_bd_N.
InterPro; IRR012928; Toxin_recpt_bd_N.
InterPro; IRR012500; Toxin_trans.
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF017923; Toxin_relans.
PRINTS; PR007923; Toxin_relans.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PF001942; ZINC PROTEASE; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium baratii.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                           Score 607; DB·1; Length 1274;
Pred. No. 1.2e-44;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0009405; P:pathogenesis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last annotation update)
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InterPro; IPR00039; Peptidase M27.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PP01742; Peptidase M27; I.
     Botulinum
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                                                                                                                                                                                                                                                                                                            Query Match 80.2%;
Best Local Similarity 83.1%;
Matches 118; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                        Toxin; Transmembrane; Zinc.
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Q45851 9CLOT PRELIMINARY;
Q45851;
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METAL
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61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                9
                                                                                                                                              1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                 ö
                                               Length 1268;
                                                                                                 22; Indels
963040091AC15ED2 CRC64;
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GO; GO:0009405; P.pathogenesis; IEA.
GO; GO:0006508; P.proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                            Query Match 76.8%; Score 581; DB 2; Best Local Similarity 76.8%; Pred. No. 2.4e-42; Matches 109; Conservative 11; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR011591; Botulinum.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001995; Pept M Zn BS.
InterPro; IPR012928; Toxin recpt_bd_N.
InterPro; IPR012500; Toxin trans.
Pfam; PF071951; Toxin R bind N; 1.
Pfam; PF07952; Toxin R bind N; 1.
PR001953; Poxin trans; 1.
PR001963; Botulinum; 1.
PR001FE; PS001963; Botulinum; 1.
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EMBL; AB037714; BAB03522.1; -; Genomic DNA.
EMBL; AB037704; BAB03512.1; -; Genomic DNA.
EMBL; AB037706; BAB03513.1; -; Genomic DNA.
EMBL; AB037706; BAB03514.1; -; Genomic DNA.
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MEDLINE=20509829; PubMed=11055954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOI=10.1128/AEM.66.11.4992-4997.2000;
                                                                                                                                                                                                                                                                                                                                                                                   121 RKNTSSNGCFWSFISKEHGWQE 142
     1268 AA; 145512 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB037709; BAB03517.1; -;
EMBL, AB037709; BAB03516.1; -;
EMBL, AB037707; BAB03515.1; -;
HSSP; Q45894; IEIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-FEB-2005 (TrEMBLrel. 29, Type E botulinum toxin.
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EMBL; AB037712; BAB03520.1
EMBL; AB037713; BAB03521.1
EMBL; AB037711; BAB03519.1
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Q9K395;
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us-08-981-087b-4.rup

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1120 RLYSGIKVKIQRVNNSSTN----DNLVRKNDQVYINFVASKTHLLPLYADTATTNKEKTI 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTRAIN=BL 6340/ATCC 43755/BL 5520/KZ 147;

MEDLINE=20509829; PubMed=11055954;

DOI=10.1128/AEM.66.11.4992-4997.2000;

MARDINE=20509829; PubMed=11055954;

DOI=10.1128/AEM.66.11.4992-4997.2000;

MARDINE X., Maegawa T., Kozaki S., Tsukamoto K., Gyobu Y.,

Mamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;

"Genetic analysis of type E botulinum toxin-producing Clostridium
butyricum strains.";

"Genetic analysis of 6:4992-4997(2000).

EMBL, ABO39264; BAB12249.1; -; Genomic_DNA.
                                       STRAIN-BL 5262;
Tsukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T., Nakamura S., Karasawa T., Kozaki S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB088207; BAC05434.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
SMR; Q6KZM3; 2-412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN 1.
41B633BB744D3B41 CRC64;
                                                                                                                                                                          GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pethogenesis; IEA.
GO; GO:0009405; P:pethogenesis; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR000395; Peptidase M27.
InterPro; IPR000395; Peptidase M27.
InterPro; IPR000405; Peptidase M27.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; BOTULINUM; I.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN I.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN I.
SEQUENCE 1252 AA; 143510 MW; 41B633BB744D3B41 CRC64
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:pathogenesis; IEA.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.7%; Score 391; DB 2; L/Best Local Similarity 55.4%; Pred. No. 1.4e-25; Matches 77; Conservative 24; Mismatches 28;
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InterPro; IPR0001395; Peptidase M27.
InterPro; IPR000035; Pept M Zn BS.
Pfam; PF01742; Peptidase M27; I.
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TNSNGFFWNFISEEHGWQE 1251
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Q9FAR6;
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      [1]
NUCLEOTIDE SEQUENCE.
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                                                                                                                 7 RLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLI 66
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                                                                                Gaps
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
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08KZM3_CLOBU FRELIMINARY; PRT; 1252 AA.
08KZM3_CLOBU (TEMBLE) 22, Created)
01-OCT-2002 (TEMBLE) 22, Last sequence update)
01-MAR-2004 (TEMBLE) 26, Last annotation update)
01-MAR-2004 (TEMBLE). 26, Last annotation update)
Name=bont/E;
Clostridium butyricum.
Bacteria Flimicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium.
NGBI_TAXID=1492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-35396;
TBukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa Nakamura S., Karasawa T., Kozaki S.;
"Sequence of the borulinum neurotoxin type E.";
"Sequence of the borulinum neurotoxin type E.";
Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.
EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
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                                         Length 1251;
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                                                                                Indels
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1251 AA; 143752 MW; 2021F4E427070296 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurotoxin type E.
                                                                                31;
                                         DB 2;
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55.4%; Pred. No. 1.8e-26;
iive 26; Mismatches 26,
                                       55.2%; Score 417.5; DB 2 55.9%; Pred. No. 6.3e-28;
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                                                                              24; Mismatches
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Q54A79;
                                                       Local Similarity 55.9 es 76, Conservative
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Matches 77; Conservative
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  SEQUENCE
                                    Query Match
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Indels 10; Gaps

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|RLYSGIKVKIQRVMNSSTN----DNLVRKNDQVYINFVASKTHLLPLYADTATTNKEKTI 1178
                                                                                                                                                                                                                                                                                                             Gimenez J.A., Dasgupta B.R.; "Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the site trypsin nicks and homology with tetanus neurotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92174922; PubMed=1541280; Whelan S.M., Blmore M.J., Boddworth N.J., Atkinson T., Minton N.P.; Whelan S.M., Elmore M.J., Boddworth N.J., Atkinson T., Minton N.P.; "The complete amino acid sequence of the Clostridium botuliuum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                                                                                                                                                                         KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN
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MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
J. Biol. Chem. 265:9153-9158(1990).
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
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MEDLINE-88197963; PubMed=3888113;
Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 419-426.
MEDLINE=90344918; PubMed=2116911; DOI=10.1016/0300-9084(90)90075-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
                                                                                                                                                         10;
                                                                                                                Length 1255;
                                                                                                                                                         28; Indels
                         Prodom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1255 AA; 143917 MW; 1B557B9D05CD0E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 183:107-113(1992)
                                                                                                             51.7%; Score 391; DB 2;
55.4%; Pred. No. 1.4e-25;
ive 24; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1250 AA
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Bur. J. Biochem. 204:657-667(1992)
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1236 TNSNGFFWNFISEEHGWQE 1254
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MEDLINE=92181428; PubMed=1543481;
                                                                                                                                                                                                                                                                                                                                                                                124 TSSNGCFWSFISKEHGWQE 142
      PR00760; BONTOXILYSIN.
                                                                                                                                                         Matches 77; Conservative
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                                                                                                                                      Local Similarity
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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J. Biol. Chem. 269:1617-1620(1994).
-!- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsyraptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptiadae that catalyzes the hydrolysis of the 180-Arg-|-Ile-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 bond in SNAP-25.
CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates COPACTOR: Binds 1 zinc ion per subunit (By similarity). SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
Jahn R., Niemann H.;
                                                                                                                                                                                                                           neurotoxin gene and
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94063091, PubMed=8243676, DOI=10.1016/0014-5793(93)80448-4; Schlavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Mehta P.P., Jontes J., Bentenina neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds.";
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PRINTS; PROUTE; BONTOXILYIN.
PROBOM; PD001963; BOLUInimm; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
3D-structure; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc. OCHAIN MET 1 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   forms of
                                                                                                 STRAIN=Type E / Hazen 36208;
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxir specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANGUS: There are seven antigenically distinct botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
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EMBL; X62683; CAA44558.1; -; Genomic_DNA.
EMBL; X70815; CAA50146.1; -; Genomic_DNA.
PIR, S208575; S08575.
PIR; S21178; S21178.
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InterPro; IPR000395; PeptIdase M27.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012500; Toxin_trans.
Pfam; PF01742; Peptidase M27; 1.
Pfam; PF07953; Toxin_R bind_N; 1.
Pfam; PF07952; Toxin_trans; 1.
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PDB; 1T3C; X-ray; A/B=1-421.
                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION OF SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF SUBSTRATE
Biochimie 72:213-217(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 335:99-103(1993)
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MEROPS; M27.002
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us-08-981-087b-4.rup

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64 KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN 123
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"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
FASEB J. 2:41750-41750(1988).
-1- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter
release. It binds to peripheral neuronal synapses, is internalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 RLYTGVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 384.5; DB 1; Length 1250;
; Pred. No. 5.2e-25;
26; Mismatches 26; Indels 11; Gaps
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MEDLINE-91237316;
MEDLINE-91237316;
MEDLINE-91237316;
Stujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.;
"Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340.";
"Gen. Microbiol. 137:519-525(1991).
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STRAIN=ATCC 43181, and ATCC 43755;
MEDLINE=92181428; bubMed=1543481;
MEDLINE=92181428; bubMed=1543481;
Boulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 44755).";
Biochem. Biophys. Res. Commun. 183:107-113(1992).
                                By similarity.

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Interchain (between light and heavy chains) (Probable).

R -5 G (in Ref. 2).

C -5 S (in Ref. 2).

R -5 A (in Ref. 2 and 3).

R -5 A (in Ref. 2 and 6).

FE -> LO (in Ref. 2 and 6).

FE -> LO (in Ref. 2 and 6).

R -> A (in Ref. 2 and 6).

R -> A (in Ref. 2 and 6).

N -> NN (in Ref. 2 and 6).

N -> NN (in Ref. 2).
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01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
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        Botulinum neurotoxin E heavy chain.
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963
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P30995;
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CONFLICT
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CONFLICT
                                    ACT SITE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc
                                  Probom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.

CHAINT MET 0 Botulinum neurotoxin R 1421 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 RLYTGVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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211 211 Zinc (catalytic) (By similarity).
215 Zinc (catalytic) (By similarity).
411 425 Interchain (between light and heavy chains) (Probable).
229 229 K -> M (in Ref. 2).
1250 AA, 143266 MW; 8171B5B2C2312857 CRC64;
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4e-24;
ches 28; ]
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54.7%; Pred. No. 4e-
                                                                                                                                                                                                                                                                                                    EMBL; X62088; CAA43998.1; -; Genomic_DNA.
EMBL; X53180; CAA37321.1; -; Genomic_DNA.
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InterPro; IPR001025; Pept M Zn BS.
InterPro; IPR0010395; Pept M Zn BS.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012500; Toxin recpt bd N.
InterPro; IPR01257; Peptidase M77; 1.
Pfam; PF07953; Toxin R bind N; 1.
Pfam; PF07952; Toxin Lans; 1.
PRINTS; PR00760; BONTOXILYSIN.
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Best Local Similarity 54.7x
Best Local Conservative
T6; Conservative
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SMR; P30995; 1-411.
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BXA1_CLOBO
ID BXA1_CLOBO
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METAL
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of botulinum neurotoxin type A.";
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MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(95)01241-5;
Rujita R., Rujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.;
"Molecular characterization of two forms of nontoxic-nonhemagalutinin components of Clostraidum botulinum type A progenitor toxins.";
FEBS Lett. 376:41-44(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Type A / NCTC 2916;
MEDLINE=90235864; PubMed=2185020;
Thompson D.E., Brehm J.K.; Oultram J.D., Swinfield T.-J., Shone C.C.,
Atkinson T., Melling J., Minton N.P.;
"The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Type A / 62A;
MEDLINE=97016817; PubMed=8863443;
MEDLINE=97016817; PubMed=8863443;
Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolyric clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J.; Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
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                            01-JUL-1989 (Rel. 11, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-
                                                                                                                                                                                                                                                                         Name=botA; Synonyms=atx, bna;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
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Biochem. Biophys. Res. Commun. 162:1388-1395(1989).
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                                                                                                                                                                                                                                chain; Botulinum neurotoxin A heavy-chain].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 1-5 AND 444-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 265:9153-9158(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84178501; PubMed=6370252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         botulinum neurotoxin type A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 1-34.
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P18639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Type A / 62A;
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1491;
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                                                                                                                                                                                                                                                                                                                                                                                           Clostridium
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Furt. Biol. 5:898-902(1998).
FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain from the hain (L) hydrolyzes the 197-cln-[-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release regults in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98455071; PubMed-9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain (H).
-!-.SUBCELLULAR LOCATION: Secreted.
-!- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the
treatment of strabismus and blepharospasm associated with dystonia
                                                                                                                                                                                       PROTEIN SEQUENCE OF 448-482.

MEDLINE=82285016; PubMed=3896784;
Shone C.C., Hambleton P., Melling J.;
"Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity.";
Eur. J. Blochem. 151:75-82(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
COFACTOR: Binds 1 zinc ion per subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
Jahn R., Niemann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                   "Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments."; J. Protein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: Binds 1 zinc ion per subunit. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds."; FRBS Lett. 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94063091; PubMed-8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.;
                                                                                               R.L.;
eavy chain into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
"Site-directed mutagenesis identifies active-site residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and A botulinal neurotoxins.";
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                                                                                                   Niece R.L.
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                                                                                                 Sathymoorthy V., Dasgupta B.R., Foley J.,
Boculinum neurotoxin type A: cleavage of
halves and their partial sequences.,
Arch. Biochem. Biophys. 266:142-151(1988).
                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
                                                             AND 872-895
terminus and around the nicking site.";
Biochimie 72:661-664(1990).
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                                                                                  MEDLINE=89024662; PubMed=3178218;
                                                                                                                                                                                                                                                                                                                                                                                                         Gimenez J.A., DasGupta B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION OF SUBSTRATE.
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                                                               PROTEIN SEQUENCE OF 448-474
                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8397793;
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1296 AA

PRT;

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                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

-!- MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, B, F, and G.
-!- SIMILARITY: Belongs to the peptidase M27 family.
-!- DATABASE: NAME-BOTOX product information Web site;
WWW-"http://www.bctox.com/site/"
-!- DATABASE: NAME-Protein Spotlight; NOTE-Issue 19 of Pebruary 2002;
WWW-"http://www.expasy.org/spotlight/back_issues/spitl019.shtml".
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Interpro; IPR000395; Peptidase M27.

Interpro; IPR000395; Peptidase M27.

Interpro; IPR012928; Toxin_respt bd_N.

Interpro; IPR012928; Toxin_respt bd_N.

Interpro; IPR012928; Toxin_respt bd_N.

Interpro; IPR012928; Toxin_respt bd_N.

Interpro; IPR012928; Toxin_respt bd_N; 1.

IPR000000; PR01953; Toxin_respt ld_N; 1.

IPR000000; PR01953; Botulinum; 1.

IPR000000; PR00142; ZINC_PR0182B; 1.

IPR05ITE; PS00142; ZINC_PR0TEASE; 1.

IPR05ITE; PS00142; ZINC_PR0TEASE; 1.

IPR05ITE; PS00142; ZINC_PR0TEASE; 1.

IPR05ITE; PS00142; ZINC_PR0TEASE; 1.

IPR05ITE; PS00142; ZINC_PR0TEASE; 1.

IPR06ITE; PS00142; TOXIN; PS00142; 1.

IPR06ITE; PS00142; TOXIN; PS00142; 1.

IPR06ITE; PS00142; TOXIN; PS00142; 1.

IPR06ITE; PS00142; TOXIN; PS00142; 1.

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E->A: Drastic decrease in enzymatic
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Botulinum neurotoxin A heavy-chain.
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Pred. No. 4.1e-18;
21; Mismatches 50; Indels 13;
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EMBL, M30196; AAA23262.1; -; Genomic_DNA.
EMBL, X92973; CAA63551.1; -; Genomic_DNA.
EMBL, D67030; BAA11051.1; -; Genomic_DNA.
EMBL, M27892; AAA23269.1; -; Genomic_DNA.
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PDB; 3BTA; X-ray; A=1-1295.
MEROPS; M27.002; -.
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RESULT 12 Q7B8V4\_CLOBO

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KIIKLIRISNSNNSLGQIIVMDS----IGNNCTMNPQNNNGGNIGLLGFHSNN----LV 111
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                                                                                                                                                                                                                                                                                                                                                                                  VUCLEOTIDE SEQUENCE.
STRAIN-Allergan-Hall A;
MEDLINE=22919384; PubMed=14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zhang L., Lin W.J., Li S., Aoki K.R.;
Complete DNA sequences of the botulinum neurotoxin complex of
Clostridium botulinum type A-Hall (Allergan) strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Gaps
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STRAIN=Type A / Kyoto-F;
MEDINE=9414363; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
MEDINE=9414363; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
Millems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison with cher clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                                            MEDLINE=22617869; PubMed=12732962; DOI=10.1007/s00284-002-3851-1; Dineen S.S., Bradshaw M., Johnson B.A.; Newrotoxin gene clusters in Clostridium botulinum type A strains: sequence comparison and evolutionary implications."; Curr. Microbiol. 46:345-352(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
13-SFP-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain].
                                                                                                      Clostridium botulinum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=botA; Synonyms=atx, bna;
Clostridium boculinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1296 AA; 149425 MW; DEABCF2754AE43E6 CRC64;
                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.5%; Score 306.5; DB 2; 44.4%; Pred. No. 4.1e-18;
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EMBL; AF461540; AAM75961.1; -; Genomic_DNA.
EMBL; AF488749; AAQ06331.1; -; Genomic_DNA.
      Created)
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                                                                 BoNT/A (Neurotoxin BoNT).
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Les 67; Conserv
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MEDLINE=22617869;
                                                                                                                                                                          NCBI_TaxID=1491;
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                                             10-MAY-2005
                                                                                                                                                        Clostridium.
                      10-MAY-2005
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East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

T. Corganization and phylosenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic clostridium toxin complex in proteolytic clostridium toxin complex in proteolytic clostridium toxin complex in proteolytic clostridium toxin complex in proteolytic clostridium toxin botulinum types A. B. and F: evidence of chimeric sequences in the gene encoding the nontroxic nonhemagglutinin component.";

Int. J. Syst. Bacteriol. 46:1106-1112(1996).

Int. J. Syst. Dacteriol. 46:1106-1112(1996).

Int. J. Syst. Dacteriol. 46:1106-1112(1996).

The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain [1] hydrolyzes the 197-Gln-|-Ag-198 bond in SNRP-25, thereby blocking results in Haccid paralysis, with frequent heart or respiratory failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTURE. Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity).

SUBCELLUIAR LOCATION: Secreted.

NISCELLANGOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.

SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure, Hydrolase, Metal-binding; Metalloprotease; Neurotoxin;
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By similarity.

By similarity.

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Interchain (between light and heavy chains) (By similarity).

By similarity.

By similarity.

Ww; 5DA04Al3D98BG372 CRC64;
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INIT MET 0 By similarity.

CHAIN 448 1295 Botulinum neurotoxin A heavy-chain.

TRANSMEM 626 646 Potential.
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PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
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EMBL; X87974; CAA61234.1; -; Genomic_DNA.
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Interpro; IPR001035; Pept dase M27.
Interpro; IPR012228; Toxin_recpt_bd_N.
Interpro; IPR012500; Toxin_trans.
Pfam; PP01742; Peptidase M27; 1.
Pfam; PP07953; Toxin_R bind_N; 1.
Pfam; PP07953; Toxin_R bind_N; 1.
                                                            PubMed=8863443;
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1295 AA; 149280
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TRANSMEM
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METAL
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Bradshaw M., Johnson E.A., Smith L.A., Marks J.D.;
Bradshaw M., Johnson E.A., Smith L.A., Marks J.D.;
"Sequence variation within botulinum neurotoxin serotypes impacts
antibody binding and neutralization.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AY953275; AAX53156.1; -; Genomic_DNA.
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Johnson B.A., Tepp W.H., Bradshaw M., Gilbert R.J., Cook P.E.,
McIntosh B.D.G.;
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Gaps

13;

51; Indels

Length 1295;

39.4%; Score 298.5; DB 1; 43.4%; Pred. No. 2.1e-17;

ilarity 43.4%; Pred. No. 2.1e-Conservative 22; Mismatches

Query Match Best Local Similarity Matches 66; Conserv

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Search completed: March 2, 2006, 00:46:26 Job time: 75.3248 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 2, 2006, 00:46:47; Search time 17.5847 Seconds Run on:

(without alignments) 672.325 Million cell updates/sec US-08-981-087B-4 757

1 NIFSNTRLYTGVEVIIRKNG......TSSNGCFWSFISKEHGWQEN 143 Title: Perfect score:

Sequence:

Scoring table:

572060 seqs, 82675679 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:\*

1. /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*

2. /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*

3. /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*

4. /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

5. /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

7. /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

6. /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Appli	Appli	Appl	Appl	Appl	Appl	Appl				Appl	Appl	Appl		', App	Appli	Appl	, App	Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appl
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	288-326A-9	US-09-548-409B-9	08-480-604A-23	08-405-496A-23	08-915-136-23	09-084-517-23	08-480-604A-26	JS-08-405-496A-26	-08-915-136-26	-09-084-517-26	-08-480-604A-28	US-08-405-496A-28	-08-915-136-28	US-09-084-517-28	US-10-360-101-219	-09-465-276-1	JS-08-446-114A-22	US-10-360-101-220	07-618-312A-2	-07-618-312A-4	08-110-786A-8	US-08-280-228-2	US-08-280-228-4	-08-668-381A-5	-08-913-880C-17	US-08-913-880C-16	913-880C-15
	-60	-09-	-98-	-08-	-80-	- 1	-08-	-08-	-08-	-60-	-80-	-08-	-89-	-60-	-10-	-60-	-08-	-10-	-07-	-01-	-080-	-80-	-08-	-08-	-08-	-80-	-80-SD
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% Query Match	40.5	40.5	40.5	40.5		40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	39.4	37.2	36.7	19.7	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1
Score	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	298.5	281.5	277.5	149	137	137	137	137	137	137	137	137	137
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Sequence 14, Appl Sequence 13, Appl Sequence 11, Appl Sequence 10, Appl Sequence 14, Appl Sequence 24925, A Sequence 3, Appli Sequence 3, Appli Sequence 570, Appl Sequence 569, Appl Sequence 19247, A Sequence 19247, A Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 71, Appli Sequence 71, Appli	-
US-08-913-880C-14 US-08-913-880C-12 US-08-913-880C-12 US-08-913-880C-11 US-08-913-880C-11 US-08-913-880C-11 US-08-913-880C-1 US-09-248-796A-22484 US-09-248-796A-22484 US-09-248-796A-22484 US-09-248-796A-230A-569 US-09-810-230A-569 US-09-810-230A-569 US-09-810-230A-569 US-09-810-316-10	
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# ALIGNMENTS

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KIIKLIRTSNSNNSLGOIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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             Sequence 9, Application US/09288326A
; Batent No. 6776990
; GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Sachs, K. Roger
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment of Pancreatitis
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment of Pancreatitis
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TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Methods and Compositions for the
TITLE REPRENCE: 17282
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 9
; SEQ ID NO 9
; LENGTH: 382
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APPLICANT: Sachs, George
TITLE OF INVENTION: Treament of Pancreatitis
FILE REPERENCE: 17282CIP(AP)
CURRENT APPLICATION NUMBER: US/09/548,409B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.5%; Score 306.5; DB 2;
Best Local Similarity 44.4%; Pred. No. 2.7e-25;
Matches 67; Conservative 21; Mismatches 50;
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APPLICANT: Steward, Lance E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Clostridium Botilinum US-09-288-326A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-548-409B-9
US-09-288-326A-9
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PATRAPHON: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESS: ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRE
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40.5%; Score 306.5; DB 2,
Best Local Similarity 44.4%; Pred. No. 2.7e-25;
Matches 67; Conservative 21; Mismatches 50;
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CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 09/288,326
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PARCSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-480-604A-23
; Sequence 23, Application US/08480604A
; Patent No. 5736139
                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Clostridium botulinum
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PRIOR APPLICATION DATA:
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APPLICANT: KINK,
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                                                                                                                                                                                                                        LENGTH: 382
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289 NIYLNSSLYRGTKFIIKKYAS---GNKDNIVRNDRVYINVVVKNKEYRLATNASQAGVE 345
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Sequence 23, Application US/08405496A
Patent No. 591966A
Patent No. 591966A
GENERAL INFORMITION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NUCLOCOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY GIBK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 10-MAR-1995
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATA: APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.5%; Score 306.5; DB 1
Best Local Similarity 44.4%; Pred. No. 3.2e-25;
Matches 67; Conservative 21; Mismatches 50
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STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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FILING DATE: 31-077-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA. DIANE E.
REGISTRATION NUMBER: 40,027
REPERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-604A-23
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US 07/985,321
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
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04-DEC-1992
                                                                                                                                                                                                                                                        : 438 amino acids
amino acid
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ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
  FILING DATE:
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                 Query Match
40.5%; Score 306.5; DB 1; Length 438;
Best Local Similarity 44.4%; Pred. No. 3.2e-25;
Matches 67; Conservative 21; Mismatches 50; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWOE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECISTRATION NUMBER: 40,027
REPERBENCE/DOCKET NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-08-405-496A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTICATION NUMBER: US 08/405,496
PILING DATE: 16-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
PRIOR PAPLICATION NUMBER: US 08/329,154
PRIOR PAPLICATION NUMBER: US 08/161,907
PILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 07/985,321
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Patent No. 6290960
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN &
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289 NIYLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVE 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 13; Gaps
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Patent No. 6613129
GENERAL INPORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
40.5%; Score 306.5; DB 3
Best Local Similarity 44.4%; Pred. No. 3.2e-25
Matches 67; Conservative 21; Mismatches 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142
                                                                                    NAME: INGOLIA, DIANE E.
REGISTRATION VUMBER: 40,027
REPERBROCK JOCKET NUMBER: 0PHD-01763
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161
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APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-480-604A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISERA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS:
ADDRESSEE: ABDLENE CARROLL, LLP STREET: 220 MONIGOMERY STREET, SUITE 2200
STARET: 220 MONIGOMERY STREET, SUITE 2200
STARET: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
40.5%; Score 306.5; DB 2; Length Best Local Similarity 44.4%; Pred. No. 3.2e-25;
Matches 67; Conservative 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
SOFTWARE: Patentin Release #1.0, Version.#1.30
SOFTWARE: Patentin Release #1.0, Version.#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-00M-1995
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
RIUN APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
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PRIOR PAPPLICATION DATE:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/POCKET NUMBER: OPHD-01610
TELEPHONE: (415) 705-4410
TELEPHONE: (415) 705-4410
TELEPHONE: (415) 705-4318
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              OPHD-01610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               LENGTH: 438 amino acids
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-09-084-517-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-08-480-604A-26
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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| GENERAL INFORMATION:
| APPLICANT: WILLIAMS, JAMES A. |
| TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM TITLE OF INVENTION: NEUROTOXIN |
| NUMBER OF SEQUENCES: 30 |
| CORRESPONDENCE ADDRESS: REDEBLES & CARROLL, LLP |
| STREET: 220 MONTGOMERY STREET, SUITE 2200 |
| CITY: SAN FRANCISCO |
| STATE: CALIFORNIA |
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATE: US/08/161,907
FILING DATE: 02-DEC-1993
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40.5%; Score 306.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 3.5e-25;
Matches 67; Conservative 21; Mismatches 50;
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PRILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTONNEY, AAGBUT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERECAMUNICATION NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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; Sequence 26, Application US/08405496A
; Patent No. 5919665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 462 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTONNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCY/DOCKET NUMBER: 09PD-01763
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
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                         US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-915-136-26
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.5%; Score 306.5; DB 1; Length 4 Best Local Similarity 44.4%; Pred. No. 3.5e-25; Matches 67; Conservative 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142.
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SAN FRANCISCO
CALIFORNIA
PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08 07/985,321
FILING DATE: 04-02C-1992

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989

ATTORNEY/AGENT INFORMATION:

NAME: INGOLIA, DIANE E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: 0PHD-01308

TELEPHONE: (415) 705-8410

TELEPHONE: (415) 705-8410

TELEPHONE: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:

LENGTH: 462 amino acide

TYPE: amino acid

TOPOLOGY: linear

MOLECTILE TYPE: protein

US-08-405-496A-26
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APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UNITED STATES OF AMERICA
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/08915136
Patent No. 6290960
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STATE:
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09084517

Patent No. 661329

GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
  Length 462;
                                                50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
40.5%; Score 306.5; DB 2; 44.4%; Pred. No. 3.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN PRANCISCO
                                                                                                                                                                                                                                                                                                 112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                                                                                                             429 ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 459
  Query Match
40.5%; Score 306.5; U
Best Local Similarity 44.4%; Pred. No. 3.5e-
Matches 67; Conservative 21; Mismatches
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US-08-405-496A-28
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| Patent No. 57461315
| Fatent No. 57461315
| Fatent No. 57461315
| GENERAL INFORMATION:
| APPLICANT: THALLEY, BRUCE S. APPLICANT: THALLEY, NISHA V. APPLICANT: PAPHYE, NISHA V. APPLICANT: PAPHYE, NOGHAR.
| APPLICANT: PIRCA, JOSEPH R. C. APPLICANT: PIRCA, JOSEPH R. C. APPLICANT: PIRCA, JOSEPH R. C. APPLICANT: PIRCA, JOSEPH R. C. APPLICANT: PIRCA, JOSEPH R. C. APPLICANT: PIRCA, JOSEPH R. C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.5%; Score 306.5; DB 2;
44.4%; Pred. No. 3.5e-25;
tive 21; Mismatches 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE, DOCKET NUMBER: 0PHD-01610
TELECOMUNICATION INFORMATION:
TELEPAONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 mmino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-007-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/9191
FILING DATE: 31-007-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 462 amino acids TYPE: amino acid
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Best Local Similarity 44.4%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-084-517-26
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US-08-480-604A-28
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1296;
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| Patent No. 591965
| GENERAL INFORMATION:
| APPLICANT: WILLIAMS, JAMES A.
| TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF INVENTION: NEUROTOXIN
| NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MEDLEN & CARROLL, LLP
| STREET: 220 MONTGOMERY STREET, SUITE 2200
| CITY: SAN FRANCISCO
| STATE: CALIFORNIA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
40.5%; Score 306.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 1.4e-24;
Matches 67; Conservative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMINICATION INFORMATION:
TELEPAONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                         PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION WUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989
ATTORNEY APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY AMBRITEN DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
  JMBER: US 08/422,711
14-APR-1995
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COMPUTER READABLE FORM:
APPLICATION NUMBER:
FILING DATE: 14-APF
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.5%; Score 306.5; DB 2; Length 1296; 44.4%; Pred. No. 1.4e-24;
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Patent No. 6613329
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
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21, Mismatches
                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
RAPPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94104
COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: INCOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OFF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                          FILING DATE:
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US-09-084-517-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, JOSEPH N.
APPLICANT: PIRCA, JOSEPH N.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
40.5%; Score 306.5; DB 1; Length
Best Local Similarity 44.4%; Pred. No. 1.4e-24;
Matches 67; Conservative 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN PRANCISCO CITY: SAN FRANCISCO COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWQE 142
                                                  PRICATION NUMBER: US 08/329,154
PRIOR PAPLICATION NUMBER: US 08/329,154
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/429,791
PRIUNG DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       OPHD-01308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
COMPUTER REALABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: BLOEDY disk
CMEDIUM TYPE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                 40,027
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: OF
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                (415) 705-8410
16-MAR-1995
                                                                                                                                                                                                                                                                                                           NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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Indels 13; Gaps

Length 848;

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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
                                                                                                                                             1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                         DB 2;
                                                  Query Match 39.4%; Score 298.5; DB 2; Best Local Similarity 43.4%; Pred. No. 5.9e-24; Matches 66; Conservative 22; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWQEN 143
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Job time : 17.5847 secs
           US-10-360-101-219
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Patent No. 686126

GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
TILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: EP 0207-060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 219
LENGTH: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KIIKLIRISNSNNSLGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 40.5%; Score 306.5; DB 2; Length 1296;
1 Similarity 44.4%; Pred. No. 1.4e-24;
67; Conservative 21; Mismatches 50; Indels 13; Gaps
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWQE 142
                                                                                FILLING JATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-DCT-1989
ATTORNEY/AGENT: 10FORMATION:
NAME: CARROLL, PETER G.
RECEISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAN: (415) 397-8338
INFORMATION FOR SEQ 1D NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-084-517-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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Best Local S:
Matches 67
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Appl Appl Appl Appl Appl

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US-10-452-024-156 US-10-452-024-127 JS-09-910-186A-14

US-11-001-241-71

Sequence Sequence Sequence

Sequence. Sequence

ALIGNMENTS

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Sequence on US/08981087A

Sequence on No. US20020081304A1

GENERAL INFORMATION:
APPLICANT: Bimore, Michael J.
APPLICANT: Minton, Nigel P.
APPLICANT: Minton, Nigel P.
APPLICANT: Titball, Richard W.
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APP
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN PC COMPATIBLE
SUFTWARE: PACENTIN Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20020081304A1th Glebe Rd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATRICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511909.5
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Crawford, Arthur R. REGISTRATION NUMBER: 25,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 143 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
STATE:
                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NIFSNTRLYTGVEVIIRKNG.........TSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
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Sequence
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'Goodata/Jybbpa/US097_PUBCOMB.pep:*
'Con2 6/ptodata/J/pubpa/US08_PUBCOMB.pep:*
'Gon2 6/ptodata/J/pubpaa/US08_PUBCOMB.pep:*
'Gon2 6/ptodata/J/pubpaa/US09_PUBCOMB.pep:*
'Gon2 6/ptodata/J/pubpaa/US10B_PUBCOMB.pep:*
'Con2 6/ptodata/J/pubpaa/US10B_PUBCOMB.pep:*
'Gon2 6/ptodata/J/pubpaa/US11_PUBCOMB.pep:*
                                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-452-024-178
US-10-130-973A-8
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                   1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                        1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                              Gaps
                                                         0,
Query Match

100.0%; Score 757; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 7.8e-68;
Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08981087A
Publication No. US20020081304A1
GENERAL INFORMATION:
APPLICANT: Blance, Michael J.
APPLICANT: Mincon, Misel P.
APPLICANT: Mincon, Nisel P.
APPLICANT: Titbachnik, Vladimir A.
APPLICANT: Titbachnik, Vladimir A.
APPLICANT: Titbachnik, Vladimir A.
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APPLICANT: Titbachnik, Vladimir A.
APPLICANT: Titbachnik, Vladimir A.
APPLICANT: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511909.5
FILING DATE: 12-JUN-1995
ATTONNEY/AGENT INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 143; Conservative 0; Mismatches 0;
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1100 No. US20020081304Alth Glebe Rd.
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COUNTRY: USA
ZIP: 22201.4741
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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Publication No. US2003009025A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROPOXIN
FILE REFERENCE: A336.6.4 067252.0107
CURRENT FILING DATE: 2001-07-20
PRIOR PELICATION NUMBER: US/09/910,186A
CURRENT FILING DATE: 2000-05-12
PRIOR PELICATION NUMBER: 60/133,865
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PRIOR PELICATION NUMBER: 60/133,975
PRIOR PELING DATE: 1999-05-12
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100.0%; Pred. No. 3.1e-67;
cive 0; Mismatches 0;
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Sequence 34, Application US/09910186A
Publication No. US20030009025A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 143; Conservative
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: US/7GB00/04644
PRIOR PILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 9926530.6
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1900-04-07
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APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.1000000
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Best Local Similarity 100.0%; Pred. No. 5.2e-67; Matches 143; Conservative 0; Mismatches 0;
100.0%; Pred. No. 3.1e-67; tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/GB02/02384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic construct US-10-130-973A-8
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                                                                                                                                                                                                                                                                                    121 RKNTSSNGCFWSFISKEHGWQEN 143
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
                        143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shone, Clifford
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                             Matches
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APPLICANT: Simpson, Lance
APPLICANT: Park, Jung-Beak
APPLICANT: Maksymowych, Andrew
APPLICANT: Maksymowych, Andrew
APPLICANT: Maksymowych, Andrew
APPLICANT: Maksymowych, Andrew
APPLICANT: Maksymowych, Andrew
APPLICANT: OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-96Ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 NIFSNITELYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 349
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         INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
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Pred. No. 3.1e-67;
                          TITLE OF INVENTION: NEUROTUAIN
FILE REFERENCE: A35626-A 067252.0107
CURRENT APPLICATION NUMBER: US/09/910,186A
CURRENT FILING DATE: 2001-07-20
PRIOR PILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 1999-06-12
PRIOR FILING DATE: 1999-05-12
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CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Synthetic Construct
US-09-910-186A-34
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                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-05-12
APPLICATION WUMBER: 60/133,869
ELING DATE: 1999-05-12
APPLICATION NUMBER: 60/133,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-05-12
APPLICATION NUMBER: 08/123,975
FILING DATE: 1993-09-21
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APPLICATION NUMBER: 60/133,868
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100.0%;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 178
LENGTH: 432
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Best Local Similarity 100.
Matches 143; Conservative
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Length 432;

DB 4;

100.0%; Score 757;

Query Match

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; OTHER INFORMATION: synthetic construct US-10-130-973A-7
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ORGANISM: Artificial sequence
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ORGANISM: Artificial Sequence
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LENGIH: 685
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US-10-478-516-6
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| Sequence 6, Application US/10478516 |
| Publication No. US20040208889A1 |
| Sequence 6, Application No. US20040208889A1 |
| GENERAL INFORMATION |
| APPLICANT: Sutton, John M. |
| APPLICANT: Shone, Clifford C. |
| TITLE OF INVENTION | Pharmaceutical Use of Secreted Bacterial Effector Proteins |
| FILE REPRENUE: 1581.1000000 |
| CURRENT APPLICATION NUMBER: US/10/478,516 |
| PRIOR APPLICATION NUMBER: PTY/GB02/02384 |
| PRIOR APPLICATION NUMBER: GB 0112687.9 |
| PRIOR FILING DATE: 2001-05-24 |
| WUMBER OF SEQ ID NOS: 32 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO S: 32 |
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OTHER INFORMATION: diphtheria toxin translocation domain with BONT/F-HC US-10-478-516-5
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100.0%; Score 757; DB 4; Length 645;
Best Local Similarity 100.0%; Pred. No. 5.2e-67;
Matches 143; Conservative 0; Mismatches 0; Indels
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Query Match

Best Local Similarity 100.0%; Pred. No. 5.3e-67;

Matches 143; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: GB 011
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 645
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ORGANISM: Artificial sequence
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RESULT

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Sequence 7, Application US/10130973A

Sequence 7, Application US/10130973A

Publication No. US20030147895A1

SEQUENCE INFORMATION:
APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Sutton, John
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.092000
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0
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US-10-478-516-7
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100.0%; Score 757; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.6e-67;
Matches 143; Conservative 0; Mismatches 0;
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Sequence 26, Application US/10478516
; Sequence 26, Application US/10478516
; Sequence 26, Application No. US20040208889A1
; GENERAL INFORMATION:
; APPLICANT: Sutton, John M.
; APPLICANT: Shone, Clifford C.
; TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
; TILE REFERENCE: 1581.100000
; CURRENT APPLICATION NUMBER: US/10/478,516
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: GB 0112687.9
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 32
; SOQTARRE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Protein sequence for YopT, factor Xa linker, diphtheria toxin OTHER INFORMATION: translocation OTHER INFORMATION: domain, with BONT/F-HC
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Pred. No. 7.7e-67;
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100.0%; Pred. No. 8.7e-67;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                        ) OTHER INFORMATION: synthetic construct US-10-130-973A-6
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 0086;
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SCOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 887
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 143; Conservative 0
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ORGANISM: Artificial sequence
                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 143; Conservative
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| Sequence 4, Application US/10130973A
| Publication No. US20030147895A1
| GENERAL INFORMATION:
| APPLICANT: Shone, Clifford
| APPLICANT: Sutton, John
| APPLICANT: Siman, Nigel
| TILLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
| FILLE REFERENCE: 1581.092000
| TILLE REFERENCE: 1581.0920000
| CURRENT APPLICATION NUMBER: US/10/130,973A
| CURRENT FILING DATE: 2002-10-21
| PRIOR PILICATION NUMBER: GB 9928530.6
| PRIOR APPLICATION NUMBER: GB 9928530.6
| PRIOR APPLICATION NUMBER: GB 008658.7
| PRIOR PILING DATE: 1999-12-02
| PRIOR PILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 4
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APPLICANT: Shone, Clifford
APPLICANT: Shone, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERBUCE: 1581.0922000
CURRENT APPLICATION NUMBER: US/10/130, 973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Synthetic construct US-10-130-973A-4
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Best Local Similarity 100.0
Matches 143; Conservative
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US-10-130-973A-6
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             Sequence 15, Application US/10130973A

Publication No. US20030147895A1

Publication No. US20030147895A1

GENERAL INFORMATION:

APPLICANT: Shone, Clifford

APPLICANT: Shone, Clifford

APPLICANT: Silman, Nigel

ITILE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/130,973A

CURRENT APPLICATION NUMBER: US/10/130,973A

CURRENT FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

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APPLICANT: Shone, Clifford
APPLICANT: Shone, Clifford
APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Slaman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR APPLICATION NUMBER: GB 09658.7
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 1092
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Best Local Similarity 100.0%; Pred. No. 9.3e-67;
Matches 143; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 1e-66;
Matches 143; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT Clostridium botulinum US-10-130-973A-15
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US-10-130-973A-15
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Job time: 56.9014 secs
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491.279 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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-10-909-769-26
-10-909-769-18
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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103.5
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Sequence 12160, A Sequence 22, Appl	Sequence 92, Appl Sequence 8, Appli	Sequence 13, Appl	8	Sequence 34, Appl	Sequence 339, App	Sequence 19, Appl	Sequence 19, Appl	Sequence 7818, Ap	Sequence 6053, Ap	Sequence 358, App	Sequence 358, App		Seguence 6480, Ap	Sequence 6752, Ap	Sequence 3774, Ap	Sequence 134, App
US-11-087-099-12160 US-10-909-769-22	US-11-052-554A-92 US-10-510-947-8	US-11-042-988-13	US-10-873-528-8	US-11-089-551A-34	US-11-052-554A-339	US-11-133-360-19	US-11-133-346-19	US-11-087-099-7818	US-11-087-099-6053	US-10-131-826A-358	US-10-973-115B-358	US-11-072-512-3810	US-11-087-099-6480	US-11-087-099-6752	US-11-087-099-3774	US-11-052-554A-134
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74.5	74.5	74	73	72.5	72	71	71	70.5	70	70	70	69.5	69.5	69.5	69.5	69.5
26 27	78 73 73	30	32	33	34	35	36	37	38	33	40	41	42	43	44	. 45

# ALIGNMENTS

RESULT 1 US/11/062 Sequence Sequence Sequence APPLIC APPLI	SULT 1 /11/062 Sequence 5, Application US/11062471A Publication No. US2005025503A1 GENERAL INFORMATION: APPLICANT: SHONE, Clifford Charles APPLICANT: SHONE, Clifford Charles APPLICANT: SHONE, Clifford Charles APPLICANT: SILMAN, Nigel TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells FILE REFERENCE: 1581.080001 TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells FILE REFERENCE: 1581.080001 CURRENT APPLICATION NUMBER: 09/831,050 PRIOR FILING DATE: 1999-11-05 FRIOR APPLICATION NUMBER: GB 98242829 FRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 11 SEQ ID NOS: 11 SEQ ID NO S. LENGTH: 1059 TITLE: PRIOR APPLICATION NUMBER: GB 98242829 TRIES PARCENTING DATE: 1998-11-05 NUMBER OF SEQ ID NOS: 11 SEQ ID NO S. LENGTH: 1059 TITLE: PRIOR APPLICATION NUMBER: GB 982428282
FEAT	FEATURE:
COTHE	; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker,
US/11/06	US/11/062,471A-5
Query Ma Best Loc Matches	Ouery Match Best Local Similarity 100.0%; Pred. No. 5.7e-68; Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
čo qa	1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNEVRKNDLAYINVVDRDVEYRLYADISIAKPE 60 
,	61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
8	
& 8	121 RKNTSSNGCFWSFISKEHGWOEN 143
8	

RESULT 2 US/11/062

Sequence Sequence Sequence

Sequence

Sequence

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Sequence 18, Application US/10909769

Publication No. US20060024331A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Sachs, George

TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterial

TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterial

TITLE OF INVENTION: 100 (ROI2003-146)

CURRENT APPLICATION NUMBER: US/10/909,769

CURRENT FILING DATE: 2004-08-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.3

SEQ ID NO 18

LENGTH: 849

TYPE: PRT

CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Lin, Wei-Jen APPLICANT: Lin, Wei-Jen APPLICANT: APPLICANT: AACH, Kel Roger APPLICANT: Sachs, George TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris FILE REPERENCE: ALLEGOLO-100 (RO12003-146) CURRENT APPLICATION NUMBER: US/10/909,769 CURRENT FILING DATE: 2004-08-02 NUMBER OF SEQ ID NOS: 34 SOUTHWARE: Patentin version 3.3 SEQ ID NO 26 ILBNGTH: 829
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        61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.0%; Score 401; DB 6; Length 829; Best Local Similarity 55.4%; Pred. No. 2e-32; Matches 77; Conservative 26; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-26
                                                                                                                                                                                                        121 RKNTSSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                                     817 RRNISSNGCFWSSISKENGWKE 838
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
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|TNSNGCFWNFISEEHGWQE 828
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ORGANISM: Artificial Sequence
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US-10-909-769-18
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Sachs, George
APPLICANT: Sachs, George
APPLICANT: Sachs, George
APPLICANT: Sachs, George
APPLICANT: Sachs, George
CURRENT APPLICATION: TOXIN COMPOUNDER: US/10/2003-146)
CURRENT APPLICATION NUMBER: US/10/2003-146)
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Version 3.3
SEQ ID NOS: 28
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                                                                             APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Shares
APPLICANT: SILMAN, Usel
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPRENDE: 1591.0800001
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPRENDE: 1591.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT APPLICATION NUMBER: US/831,050
PRIOR PILING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 8
LENGTH: 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 757; DB 7; Length 1084; Best Local Similarity 100.0%; Pred. No. 5.8e-68; Matches 143; Conservative 0; Mismatches 0; Indels 0.
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80.2%; Score 607; DB 6;
Best Local Similarity 83.1%; Pred. No. 4.6e-53;
Matches 118; Conservative 8; Mismatches 12.
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Sequence 8, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
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Publication No. US20060024331A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60

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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
APPLICANT: Sachs, George
APPLICANT: Acki, Kei Roger
APPLICANT: ALESONID-100 (ROIZO03-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT PILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
LIENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M
US/11/062,471A-6
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells; FILE REFERENCE: 1581.080001 us/11/062,471A CURRENT APPLICATION NUMBER: 105/11/062,471A CURRENT APPLICATION NUMBER: 09/831,050 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR PRILING DATE: 1998-11-05 PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRILING DATE: 1998-11-05 PRIOR PRINGE PRINGE DATE: 1998-11-05 PRIOR PRINGE PRINGE PRINGE PRINGE DATE: 1998-11-05 PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE PRINGE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.5%; Score 306.5; DB 7;
44.4%; Pred. No. 8.2e-23;
vative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1059 ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10909769; Publication No. US20060024331A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 29.2%
Matches 47; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    918 NIYLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVE 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KIIKLIRTSNSNNSLGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
                                                                                                                                                                                                                                                                                                                    APPLICANT: STUTON, JOHN Mark
APPLICANT: STUMN, JOHN Mark
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFRENCE: 1581.080001
CURRENT FILING DATE: 1005-02-22
FRIOR FILING DATE: 1999-11-05
PRIOR PELICATION NUMBER: 09/831,050
PRIOR PELICATION NUMBER: PCT/GB99/03699
PRIOR PELICATION NUMBER: GB 9824282.9
PRIOR PELING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR PELING DATE: 1999-11-05
SOFTWARE: PACHILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SSCT IN NO 3
LENGTH: 1067
                                                                                                                                                                                                                                                                                                                                                                                                 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
                                                                                                                                                                                                                                                                           1 NIFSNITRLYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
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                                                                                                                                                        ; Score 306.5; DB 6; Length 1; Pred. No. 6.1e-23; 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.5%; Score 306.5; DB 7; Best Local Similarity 44.4%; Pred. No. 8e-23; Matches 67; Conservative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1034 ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWOE 142
                                                      ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/11062471A Publication No. US20050255093A1
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APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                        40.5%;
ilarity 44.4%;
Conservative 2
                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                  67;
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Best Local S
Matches 67
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                                   FEATURE:
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Gaps

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NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2
SEQ ID NO 7
                                                                                           TYPE: PRT
ORGANISM: Artificial
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                                                                      LENGTH: 1095
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US/11/062,471A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800 EKLFLSIISDSNEFYKTIEIKEYDEQPSYSCQLLFKKDERSTDDIGLIGIHRFYESGVLR 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: 09/831,050
PRIOR PPLING DATE: 1999-11-05
PRIOR PPLING DATE: 1999-11-05
PRIOR PPLING DATE: 1999-11-05
PRIOR PPLING DATE: 1998-11-05
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PRIOR PELING DATE: 1998-11-05
SPING PLING DATE: 1998-11-05
SPING PELING DATE: 1998-11-05
SPING PLING DATE: 1998-11-05
SOFTWARE: PATENTIN VOS: 11
SOFTWARE: PATENTIN VOS: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, NIGEL
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1005-02-22
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
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                                                                                                860 KKYKDYFCISKWYLKEVKRKPYKSNLGCNWQFIPKDEGWTE 900
                                                                 107 ---SNNLVASSWYYNNI-RKNTSSN-GCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 ISNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH-
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                                                                                                                                                                                                                          Sequence 4, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 41; Conserv
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Abi, Wel-Jen
APPLICANT: Abi, Wel-Jen
APPLICANT: Achi, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris
FILE REFERENCE: ALLE0010-100 (ROI2003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 3.0
LENGTH: 855
OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
                                                                                                                                                                                                                                                                                                                                          8 LYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIR 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 855;
                                                                                 19.7%; Score 149; DB 7; Length 1095; 26.6%; Pred. No. 5e-07;
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                                                                                                                                                                                                                                                                                                          68 TSNSNNSLGQIIVM --- DSIGNNCTMNFQNN -- NGGNIGLLGFH-
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18.8%; Score 142.5; DB 6;
Best Local Similarity 25.6%; Pred. No. 1.7e-06;
Matches 42; Conservative 25; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 VASSWYYNNIRKN--TSSNGCFWSFISKEHGWQE 142
                                                                                                                                        28; Mismatches
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; Sequence 141, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
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Sequence 30, Application US/10909769

Publication No. US20060024331A1

GENERAL INFORMATION:
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                                                                              Query Match
Best Local Similarity 26.6*
Matches 41; Conservative
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Sequence 171, Application US/11052554A
Publication No. US20050288866A1
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
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                                                                                                                                                                                                735
                                                                                                                                                                                                                                                              59 PEKIIKLIRISNSNNSLGQIIVMDSIGNNCTMNF-----QNNNGGNIGLLGFHSNNLVAS 113
                                                                                                                                                                                                                                                                                                                                                                                                    ----SNGCFWSFISKEHG 139
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                                                                                                                                  6 TRLYTGVEVIIR----KNGSTDISNTDNFVRK---NDLAYINVVDRDVEYRLYADISIAK
                                                                                                                                                                        Gaps
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                                                                 79;
Length 834;
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Pred. No. 0.44;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 10263
13.7%; Score 103.5; DB 6;
.larity 21.9%; Pred. No. 0.013;
Conservative 22; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Sco. 28.5%; Pred. No. v.. 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10263, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Clostridium acetobutylicum
US-11-087-099-10263
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 171
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Best Local Similarity
                                     Best Local Similarity
Matches 40; Conserv
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APPLICANT: Steward, Lance B.
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APPLICANT: Stancombe, Patrick
APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR APPLICATION NUMBER: 09/255,829
DR FILING DATE: 1999-02-23
DR FILING DATE: 1997-08-22
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 08/782,893
DR PILING DATE: 1996-12-27
DR FILING DATE: 1996-12-27
DR APPLICATION NUMBER: GB9625996.5
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR FILING DATE: 2002-09-12
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APPLICATION NUMBER: GB9617671.4
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Publication No. US20060024331A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1997-06-22
PRIOR FILING DATE: 1997-06-22
PRIOR PELING DATE: 1996-12-27
PRIOR FILING DATE: 1996-12-17
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SOFTWARE: Patentin version 3.1
SEQ ID NO 141
LENGTH: 1315
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US-11-077-550-141
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| LENGTH: 2340
| TYPE: PRT | CARANISM: Rickettsia prowazekii | TYPE: PRT | CARANISM: Rickettsia prowazekii | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11-052-554A-171 | US-11
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